

CC sequences, a NotI restriction site, a ribosome binding site (RBS), a
 CC pElB leader, a spacer region, a cloning region bordered by 5' XhoI and
 CC 3' SpeI restriction sites, the tetracycline resistance gene encoding
 CC bacteriophage cp3 followed by a stop codon, a NheI restriction site
 CC between the two cassettes, and a second lacZ promoter/operator sequence,
 CC followed by an expression control RBS, a pElB leader, a spacer region, a
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the MT4 Fab display phagemid expression vector, pMT4-3 (see also
 CC Q92540), used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV. 1170 A; 1171 C; 1232 G; 1118 T;
 CC Sequence 4691 BP; 1170 A; 1171 C; 1232 G; 1118 T;

Query Match 83.0%; Score 263; DB 16; Length 4691;
 Best Local Similarity 91.2%; Pred. No. 4 10e-160;
 Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 2674 gccagctcacgactccagggaccctcttctgtctccagggaaagagccacctc 2733
 CC |||||||
 QY 1 GCGAGCTCACGAGCTCCAGGACCTCTGTCTGTCTCCAGGGGAAAGAGCCCTC 60
 CC |||||||
 Db 2734 tctgcaggccagctcacagttatagcaggccctacttagctgtaccagcagaacct 2793
 CC |||||||
 QY 61 TCTGCAGGCGCAGTCAGAGCTTTAGCAGCAATACITAGCTGTGTTACCAACAGAACT 120
 CC |||||||
 Db 2794 gccaggtccaggtctctctctatgtgtacatccagcaggccactggtccatccagac 2853
 CC |||||||
 QY 121 GGCAGGCTCCAGGCTCTTCAATATATCATGATCCAGCAGGAGTATGTCATGCCAGAC 180
 CC |||||||
 Db 2854 aggttcagtgagcagggtgggtctgggacagactctcactccatccagcagcaggacct 2913
 CC |||||||
 QY 181 AGTTCAGTCGAGCAGTGGGCTCTGGAGACACATCTCAGCTCCAGCATCAGCAGATTTGAGCT 240
 CC |||||||
 Db 2914 gaagatttgcagctatctactgttcagcagctatgtgtgctcagctggttcggcccaagg 2973
 CC |||||||
 QY 241 GAAGATTTTGCAGCTATTACTGTCTAGCAGTATGAGCAGTATGAGCAGCTCTGAGCAGAGG 300
 CC |||||||
 Db 2974 accaaggtggaactcaaa 2991
 CC |||||||
 QY 301 ACCAAGGTGGAATCAAA 318

RESULT 2
 ID Q92547 standard: DNA; 6166 BP.

AC Q92547;
 DT 11-MAR-1996 (first entry)
 DE Expression vector, pPho-IT.
 KW Human; Fab; variable chain, heavy, light, region, VH, VL, HIV, gp120,
 KW 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; MAB;
 KW immunoreaction; neutralisation; passive immunotherapy; tetanus toxin;
 KW alkaline phosphatase; phoA; ss; cyclic.
 OS Synthetic
 PN W09511317-A1
 PF 27-APR-1995.
 PP 19-OCT-1994; U11907.
 PR 19-OCT-1994; US-130409
 PR 26-APR-1994; US-233619
 PR 19-SEP-1994; US-308841.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 95-170235/22.
 PT Synthetic human neutralising monoclonal antibodies to human
 PT immunodeficiency virus - used for diagnosis and immuno:therapy of
 PT HIV-induced disease
 PT Example 2; Page 193-197; 249pp; English.
 CC This sequence represents the expression vector, pPho-IT which is a
 CC modified version of the phagemid expression vector, pComb3 given in
 CC Q92546. pPho-IT provides for the expression of soluble Fabs which are
 CC secreted into the periplasmic space which is regulated from the alkaline
 CC phosphatase (phoA) promoter. This plasmid was used within the scope of
 CC the invention to express various mutagenised human Fab's which comprise
 CC heavy and light variable regions which bind to HIV gp120. pPho-IT

CC consists of a DNA molecule having two cassettes to express two soluble
 CC proteins a heavy chain and a light chain. The vector comprises,
 CC operatively linked 5' to 3', a first cassette consisting of the phoA
 CC promoter/operator sequences, an EcoRI restriction site, a ribosome
 CC binding site (RBS), an OmpA leader, a SfiI restriction site, a spacer
 CC region, a cloning region bordered by 5' sacI and 3' XbaI restriction
 CC sites, an NcoI restriction site between the two cassettes, and a second
 CC cassette consisting of an expression control RBS, a pElB leader, a human
 CC consensus amino terminus spacer region comprising the sequence EVGLLE,
 CC a cloning region bordered by 5' XhoI and 3' SpeI restriction sites
 CC followed by a SfiI site, expression control stop sequences and a NotI
 CC restriction site. The pPho-IT expression vector contains a light
 CC chain stuffer that is 1200 bp in length and a heavy chain stuffer that
 CC is 300 bp in length. The nucleotide sequences of the heavy and light
 CC chain stuffer encode the heavy and light chain variable domains of a
 CC tetanus toxin-specific Fab.
 CC Sequence 6166 BP; 1416 A; 1706 C; 1629 G; 1415 T;

Query Match 83.0%; Score 263; DB 16; Length 6166;
 Best Local Similarity 91.2%; Pred. No. 3.10e-160;
 Matches 240; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 4604 gccagctcacgagctccagggaccctctgtctctccagggaaagagccacctc 4663
 CC |||||||
 QY 1 GCGAGCTCACGAGCTCCAGGACCTCTGTCTGTCTCCAGGGGAAAGAGCCCTC 60
 CC |||||||
 Db 4664 tctgcaggccagctcacagttatagcaggccctacttagctgtaccagcagaacct 4723
 CC |||||||
 QY 61 TCTGCAGGCGCAGTCAGAGCTTTAGCAGCAATACITAGCTGTGTTACCAACAGAACT 120
 CC |||||||
 Db 4724 gccaggtccaggtctctctctatgtgtacatccagcagggccactggtccatccacac 4783
 CC |||||||
 QY 121 GGCAGGCTCCAGGCTCTTCAATATATCATGATCCAGCAGGAGTATGTCATGCCAGAC 180
 CC |||||||
 Db 4784 aggttcagtgagcagggtgggtctgggacagactctcactctcagcagcagctgagct 4843
 CC |||||||
 QY 181 AGTTCAGTCGAGCAGTGGGCTCTGGAGACACATCTCAGCTCCAGCATCAGCAGATTTGAGCT 240
 CC |||||||
 Db 4844 gaagatttgcagctatctactgttcagcagctatgtgtgctcagctggttcggcccaagg 4903
 CC |||||||
 QY 241 GAAGATTTTGCAGCTATTACTGTCTAGCAGTATGAGCAGTATGAGCAGCTCTGAGCAGAGG 300
 CC |||||||
 Db 4904 accaaggtggaactcaaa 4921
 CC |||||||
 QY 301 ACCAAGGTGGAATCAAA 318

RESULT 3

ID T15203 standard: cDNA; 646 BP.
 AC T15203;
 DT 23-OCT-1996 (first entry)
 DE p3AP313 anti-tetanus toxoid Ig light chain variable domain cDNA.
 KW Mutagenesis; Ig; immunoglobulin; FR; framework region; variable; CDR;
 KW complementarity determining region; light; heavy chain; PCR;
 KW polymerase chain reaction; antibody library; diversity; affinity;
 KW immunospecificity; ss.
 OS Synthetic
 PN W09607754-A1.
 PD 14-MAR-1996.
 PP 01-SEP-1995; U11235.
 PR 02-SEP-1994; US-300386.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-171625/17.
 PT Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
 PT gene CDR - useful for prodn. of Ig heavy and light chain
 PT combinatorial antibody libraries
 PS Example 1; Page 84; 125pp; English.
 CC T15202 and T15203 are the heavy and light chain variable domains of
 CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a pComb3
 CC based expression vector. The heavy and light chain variable domains
 CC are used in an example to demonstrate the prodn. of antibodies for
 CC an antibody library using mutagenic primers. Mutagenic primers of the

CC invention have sequences at their 3' and 5' ends both capable of
 CC binding different framework regions linked by a sequence 6 to 50
 CC nucleotides long different immunoglobulins produced using the
 CC primers can be used to produce antibody libraries having diverse and
 CC novel immunospecificities and affinities. By using mutagenic ONS an
 CC extremely large population of different randomised binding sites can
 CC be created and use of the universal light chain increases the number
 CC of combinations which yield functional heterodimeric antibodies.
 SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T;

Query Match 81.4%; Score 258; DB 22; Length 646;
 Best Local Similarity 90.8%; Pred No 9 346-157;
 Matches 266; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 1 gagctcagcagcttcacagcaccctctctttctccaggggaaagagccacctctcc 60
 |||||
 QY 4 GAGCTCAGCAGCTTCACGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 63
 |||||
 Db 61 tgcagggccagcttcacagcagcttcacagcagcttcacagcagcttcacagc 120
 |||||
 QY 64 TGCAGGGCCAGCTTCACGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123
 |||||
 Db 121 cagactccagcagcttcacagcagcttcacagcagcttcacagcagcttcacag 180
 |||||
 QY 124 CAGACTCCAGCAGCTTCACGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 183
 |||||
 Db 181 tccagtcagcagcttcacagcagcttcacagcagcttcacagcagcttcacag 240
 |||||
 QY 184 TTCAGTCCAGCAGCTTCACGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 243
 |||||
 Db 241 gattttcagctgactatcagcagcagcttcacagcagcttcacagcagcagc 300
 |||||
 QY 244 GATTITCAGTGTAATTCAGCAGCAGTATGSAACACCTCTGACCTTCGCCGCG 303
 |||||
 Db 301 aagctgaaactcaaa 315
 |||||
 QY 304 AAGGTGGAATCAAA 318
 |||||

RESULT 4
 ID Q70487 standard; cDNA: 646 BP.
 AC Q70487;
 DT 04-APR-1995 (first entry)
 DE Anti-tetanus toxoid light chain CDNA from vector, pC3AP313.
 KW Polymerase chain reaction; primer; mutagenesis; PCR; amplify;
 KW diversity; antibody; complementarity determining region; CDR;
 KW framework; constant; light; heavy; phase; immunoglobulin; library; ss.
 OS Synthetic.
 FN W09418213.6.
 PD 18-AUG-1994
 PF 02-FEB-1994; J01234.
 PP 02-FEB-1993; US-012566.
 PR 28-DEC-1993; US-174674.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DP, Ierner PA;
 DR WPI: 94-279673/34.
 FT Oligo-nucleotides - used as PCR primers for producing increased
 FT diversity antibody libraries, for screening antigens
 PS Claim 21: Page 84-85; 120pp; English.
 CC This sequence represents the light chain coding sequence derived from
 CC the surface display phagemid expression vector, pC3AP313.
 CC contains the bacteriophage gene III and heavy and light chain variable
 CC domain sequences for encoding human Fab antibodies against tetanus toxin
 CC This sequence was pref used in the method of the invention for the
 CC production of antibody libraries containing increased diversity. The
 CC sequences given in Q70480-86 are primers which were used for inducing
 CC mutagenesis in a complementary determining region (CDR) of an
 CC immunoglobulin light chain gene. These primers contain a 3' terminus
 CC capable of hybridising to a first framework region, a 5' terminus
 CC capable of hybridising to a second framework region and a nucleotide
 CC sequence between the 5' and 3' termini having the formula (NKK)n,
 CC where n is 3-24. These primers may be used to produce antibody
 CC libraries with increased antibody diversity by inducing mutagenesis

CC within the CDP regions of immunoglobulins heavy or light chains that
 CC are displayed on the surface of filamentous phage particles comprising
 CC the library. These primers pref mutate the light chain CDR1.
 SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T;

Query Match 81.4%; Score 258; DB 12; Length 646;
 Best Local Similarity 90.8%; Pred No 9 346-157;
 Matches 266; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 1 gagctcagcagcttcacagcaccctctctttctccaggggaaagagccacctctcc 60
 |||||
 QY 4 GAGCTCAGCAGCTTCACGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 63
 |||||
 Db 61 tgcagggccagcttcacagcagcttcacagcagcttcacagcagcttcacagc 120
 |||||
 QY 64 TGCAGGGCCAGCTTCACGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123
 |||||
 Db 121 cagactccagcagcttcacagcagcttcacagcagcttcacagcagcttcacag 180
 |||||
 QY 124 CAGACTCCAGCAGCTTCACGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 183
 |||||
 Db 181 tccagtcagcagcttcacagcagcttcacagcagcttcacagcagcttcacag 240
 |||||
 QY 184 TTCAGTCCAGCAGCTTCACGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 243
 |||||
 Db 241 gattttcagctgactatcagcagcagcttcacagcagcttcacagcagcagc 300
 |||||
 QY 244 GATTITCAGTGTAATTCAGCAGCAGTATGSAACACCTCTGACCTTCGCCGCG 303
 |||||
 Db 301 aagctgaaactcaaa 315
 |||||
 QY 304 AAGGTGGAATCAAA 318
 |||||

RESULT 5
 ID Q49155 standard; cDNA: 387 BP.
 AC Q49155;
 DT 01-NOV-1993 (first entry)
 DE F105 rearranged variable region light chain.
 KW Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;
 KW C104; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency; ss.
 OS Homo sapiens.
 FN Key Location/Qualifiers
 FT sig_peptide 1..57
 FT /tag= a
 FT mat_peptide 58..387
 FT /tag= b
 FN W09312232.6.
 PD 24-JUN-1993.
 PF 10-DEC-1992; U10928.
 PP 10-DEC-1991; US-804652.
 PA (DAND) DANA FABER CANCER INST INC.
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 PI Haseltine WA, Marasco WA, Posner MP, Sodroski JG;
 DR WPI: 93-214174/26.
 DR P-PSDB: R41286.
 FT DNA segments encoding monoclonal antibody - which binds to gp120
 FT and neutralises HIV, for treating AIDS, and for diagnosing and
 FT monitoring HIV infection
 PS Claim 1: Page 79; 109pp; English.
 CC mRNA from the known hybridoma F105 was converted to cDNA and this
 CC subjected to PCR amplification using primers corresp. to appropriate
 CC parts of the heavy or light chains and having restriction sites to
 CC permit cloning. The extension products were isolated and sequenced.
 CC The recombinant human monoclonal antibody (MAb) binds to a
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein. This
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad
 CC range of HIV isolates. The MAb may be used to treat immune
 CC deficiency, esp. at doses of 0.1-10 mg/kg.
 SQ Sequence 387 BP, 88 A, 111 C, 101 G, 87 T;

Query Match 79.5%; Score 252; DB 7; Length 387;

Best Local Similarity 92.6%; Pred. No. 1.39e-152;
Matches 289; Conservative 0; Mismatches 20; Indels 3; Gaps 2;

Db 73 acgcagctccagaccctctgtttgtctgcaggggaaagagaccacctctctgcagg 132
|||||
Qy 10 AGGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAGAGACACCTCTCTCTGCGAGG 59
|||||

Db 133 gccagtcagagtgtagcagcaggtactctagcctgtgtaccagcagaaacctggccaggct 192
|||||
Qy 70 GCCAGTCAGAGTCTTAGCAGCAATACTTAGCNTGTGTACCAACAGAAACTCTGCCAGGCT 129
|||||

Db 193 cccaggtccctcatctatgtgtgcatccagcagggccactggcatccagcagaggttcagt 252
|||||
Qy 130 CCCAGGCTCTTCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189
|||||

Db 253 gccagtggtctgggacagacactctcactctcaccatcagcagagtgagcctgaagatttt 312
|||||
Qy 190 GGCAGTGGGTCTGGACAGAGACITTCACITCTCAGCATCAGCAGATTTGGAGCCTGANGATTIT 249
|||||

Db 313 gcagtgattactctcagcgaatatgtatactccgtttgtacttttggccaggggacccaag 372
|||||
Qy 250 GCAGTGATTACTCTCAGCAGATGATGG-AACACC--TCGACCTTCGGCCAGGGGACCAAG 306
|||||

Db 373 ctggagatcaaa 384
|||||
Qy 307 GTGGAATCAAA 318
|||||

RESULT 6
ID N81637 standard; DNA; 1011 BP.
AC N81637;
DT 07-JAN-1991 (first entry)
DE Anti-pseudomonas aeruginosa human type antibody L-chain coding DNA
DE contg. constant region of kappa and lambda types
KW Pseudomonas aeruginosa F4; Pseudomonas aeruginosa HI;
KW immunotherapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT TATA_signal 264..271
FT /*tag= a 325..559
FT CDS 325..559
FT /*tag= b 325..571
FT misc_feature 325..571
FT /*tag= c 560..895
FT /*note= "L" 560..895
FT CDS 560..895
FT /*tag= d 572..856
FT /*note= "P81245" 572..856
FT misc_feature 572..856
FT /*tag= e 857..895
FT /*note= "V" 857..895
FT misc_feature 857..895
FT /*tag= f 572..856
FT /*note= "J" 572..856
FT misc_feature 572..856
FT /*tag= g 572..856
FT /*note= "Claimed SQ" 572..856
PN J63152984-A.
PD 25-JUN-1988.
PE 20-MAR-1987; 064183
PP 18-AUG-1986; JP-191687
PA (WAKU-) Wakunaga Selyaku KK.
WPI: 88-215877/31.
DR P-PSDB; P81246, P81245.
DR Anti-pseudomonas aeruginosa type antibody L-chain coding DNA -
PT contains constant kappa and lambda type regions, and versatile
PT region recognising ps.aeruginosa F4 and HI types
PS Disclosure: Pages 610-611; 12pp; Japanese.
CC It also codes for a variable region recognising Ps.aeruginosa F4 and HI
CC types. The Ab can be used for immunologic control of infection caused by
CC Ps.aeruginosa. The antibody is made effective against various classes or

CC subclasses of resistant Ps aeruginosa by recombining corresp DNA L-chain
CC contg. versatile coding region.
SQ Sequence 1011 BP; 237 A; 263 C; 254 G; 257 T;

Query Match 78.9%; Score 250; DB 1; Length 1011;
Best Local Similarity 90.3%; Pred No. 3.41e-151;
Matches 279; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 584 acgcagctccagaccctctgtttgtctgcaggggaaagagaccacctctctgcagg 643
|||||
Qy 10 ACCCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAGAGACACCTCTCTCTGCGAGG 59
|||||

Db 644 gccagtcagagtgtagcagcaggtactctagcctgtgtaccagcagaaacctggccaggct 703
|||||
Qy 70 GCCAGTCAGAGTCTTAGCAGCAATACTTAGCNTGTGTACCAACAGAAACTCTGCCAGGCT 129
|||||

Db 704 gccaggtctctcatctatgtgtgcatccagcagggccactggcatccagcagaggttcagt 763
|||||
Qy 130 CCAGAGCTCTTCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189
|||||

Db 764 gccagtggtctgggacagacactctcactctcaccatcagcagagtgagcctgaagatttt 823
|||||
Qy 190 GGCAGTGGGTCTGGACAGAGACITTCACITCTCAGCATCAGCAGATTTGGAGCCTGANGATTIT 249
|||||

Db 824 gcagtgattactctcagcgaatatgtatactccgtttgtacttttggccaggggacccaagttg 883
|||||
Qy 250 GCAGTGATTACTCTCAGCAGATGATGG-AACACC--TCGACCTTCGGCCAGGGGACCAAG 809
|||||

Db 884 gacatcaaa 892
|||||
Qy 310 GAAATCAAA 318
|||||

RESULT 7
ID N91359 standard; DNA; 1011 BP.
AC N91359;
DT 02-MAR-1990 (first entry)
DE Anti-P. aeruginosa strain F4 light chain V and J coding regions
KW Immunoglobulin.
OS Pseudomonas aeruginosa F4.
FH Key Location/Qualifiers
FT CDS 325..372
FT /*tag= a 560..895
FT CDS 560..895
FT /*tag= b 264..271
FT TATA_signal 264..271
FT /*tag= c 560..895
PN J01211498-A.
PD 24-AUG-1989.
PP 19-FEB-1988; 035395.
PP 19-FEB-1988; JP-035395.
PA (WAKU) Wakunaga Selyaku KK.
DR WPI: 89-303485/42.
DR P-PSDB; P91001.
DR Production of human IgG monoclonal antibody - by converting human
PT antibody into other subclasses by genetic engineering
PS Disclosure: fig. 3; 17pp; Japanese.
CC This encodes a variable chain and can be connected to a gene encoding
CC a constant region which determines optional Igg subclass. This can be
CC used to study subclasses, and as an antigen for prep. IgG1 or IgG3
CC antibody. Regions 325-372 connected to 460-571 encode the L chain.
CC region 572-856 encodes V chain and region 857-895 encodes J chain.
SQ Sequence 1011 BP; 237 A; 263 C; 254 G; 257 T;

Query Match 78.9%; Score 250; DB 1; Length 1011;
Best Local Similarity 90.3%; Pred. No. 3.41e-151;
Matches 279; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Db 584 acgcagctccagaccctctgtttgtctgcaggggaaagagaccacctctctgcagg 643
|||||
Qy 10 ACCCAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAGAGACACCTCTCTCTGCGAGG 59
|||||

Db 644 gccagtcagagtgtagcagcaggtactctagcctgtgtaccagcagaaacctggccaggct 703
|||||

	Matches	256:	Conservative	0:	Mismatches	10:	Indels	0:	Gaps	0:
Ddb	375	acgcagctccagcagccctgtctt	gtctccagggaaagcaccctctctgcag	434						
QY	10	ACGCAGTCTCCAGCACCCCTGT	CTTTGTCTCCAGGGAAAGACGACCTCTCTCGAG	69						
Ddb	435	gccagtcagagtttagcagcaact	cttagccttagtaccagcagaacctgcccagct	494						
QY	70	GCCAGCTCAGACTCTTAGCAG	AAATACCTTAGCTGTGTACCAACGAACCTTGGCCAGGCT	129						
Ddb	495	cccaggtcctcatctatgctgc	atccagcaggggccatcggtcatccagacaggttcagt	554						
QY	130	CCCAGGCTCTTCATTATGAT	GTGATCCACAGGGGCACTGGCATCCAGACAGAGTTCAGT	189						
Ddb	555	ggcagtaggcttaggcagaactt	ctactctcacatcagcacagcaggagctgaagatttt	614						
QY	190	GGCAGTGGGCTTGGACAGAC	TTTACCTCTACGATCACAGCATTCAGAGATTTGAGATTTT	249						
Ddb	615	gcadtgtattactgtcagcagat	gtgg	640						
QY	250	GCAGTGTATTACTCTCAGCA	GTATGG	275						

RESULT	ID	Accession	Source	Organism	Gene	Protein	Location/Qualifiers
	T37182	standard	DNA	900 BP			
AC	T37182						
DE	14-APR-1997	(first entry)					
DE	DNA fragment vk65.8	containing variable kappa chain gene.					
DE	Variable: kappa chain; gene segment: human; DNA fragment: vk65.8;						
DE	unrearranged; light chain; minilocus; transgenic; mouse;						
DE	production; heterologous; antibody; gamma; immunoglobulin; ss.						
OS	homo sapiens.						
Key	Key	Location/Qualifiers					
FT	exon	116..164					
FT	/*tag= a						
FT	exon	352..550					
FT	/*tag= b						
PN	US5545806.A						
PD	13-AUG-1996						
PF	24-AUG-1990	574749					
PF	29-AUG-1990	US-574748					
PPR	31-AUG-1990	US-575962					
PPR	17-DEC-1991	US-810279					
PPR	18-MAR-1992	US-853408					
PPR	23-JUN-1992	US-904068					
PPR	16-DEC-1992	US-990860					
PPA	(GENP-) GENPHARM INT INC.						
PPI	Kay RM; Lonberg N;						
PPI	WPI: 96-383736/38.						
PPT	p-PSD8; W03948.						
PPT	prodn. of heterologous human immunoglobulin(s) - by immunising						
PPT	transgenic mice						
PPT	Example 21; Fig 43: 94pp; English.						
CCC	The present sequence is the variable kappa chain gene segment						
CCC	containing human DNA fragments, vk65.8, which was co-injected along						
CCC	with the human DNA fragments vk65.3, vk65.5 and vk65.15 into half						
CCC	day mouse embryo pronuclei, to generate an unrearranged light chain						
CCC	minilocus transgene. The resulting transgenic mice can be used for						
CCC	the production of heterologous (i.e. human) antibodies against						
CCC	specific antigens, this comprises immunising a mouse with a						
CCC	preselected antigen and collecting antigen binding heterologous						
CCC	human gamma immunoglobulins.						
CSQ	Sequence 900 BP; 220 A;						
CSQ	Sequence 900 BP; 201 C; 238 T						

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Query March      77 98: Score 247; DB 27; Length 900;
Best Local Similarity 96.29; Pred No. 4 150-149;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Db      375  acgcagctccaggacacccctgtttgtccaggggaaagacacccctctcgcag 434
      |||||
      10  ACGCAGCTCCAGACACCTGTCTTGTCTCAGSSAAAGACACCTCTCTGTCAGS 69
      |||||
      Db      435  gccagtcagagctgtatgacacagctacttagcctggtaccagcgaagaacctggccaggct 494

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70	GCACGTCAGATCTTACGACAAATACCTTAGGATGAGTATACAGAAATTTGATATAGCT	129
QY		
495	ccaggtccctcatctatggtgcatccagcaggccactggcatcccgacagattcaggt	554
Db		
130	CCACAGCTCTCTATTATGATGATCATCAAGGCTATATGTCATGCTACAGGTTTAT	189
QY		
555	ggcaatgggtctggacagacttcactccacatccacagactgaagacctgaagatttt	614
Db		
190	GGATGAGGCTGTGGAGACATCTACTCTACATCAGACAGATTCGAGGCTGAGATTTT	249
QY		
615	gcagtgattactgcagcagtagtg	640
Db		
250	GCAGTGATTACTCTCAGCAGTAGG	275
QY		

RESULT	11	
ID	Q42707 standard; DNA; 390 BP.	
AC	Q42707;	
DT	01-NOV-1993 (first entry)	
DE	F105Vk-F105Jk.	
KW	Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;	
KW	CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;	
KW	chain; epitope; immune deficiency; ss.	
OS	Homo sapiens.	
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FT	/label= CDR2	
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PD	24-JUN-1993.	
PR	10-DEC-1992; U10928.	
PR	10-DEC-1991; US-804652.	
PPA	(DAND) DANA FABER CANCER INST INC	
PPA	(NWE-) NEW ENGLAND DEACONESS HOSPITAL CORP.	
PI	Haseltine WA, Marasco WA, Posner MR, Sodroski JG;	
DR	WPI: 93-214174/26.	
DR	P-PSDB: R38672.	

P-Subst: K36071Z.
DNA segments encoding monoclonal antibody - which binds to gp120
and neutralises HIV, for treating AIDS, and for diagnosing and
monitoring HIV infection
PS Disclosure: page 73-74: 109pp: English.
CC The nucleotide sequence of F105 Vp (Q42707 - sequence differs from
other F105 Vp sequences given elsewhere in the specification) was
compared with germline gene HumvK325 (Q42708), showing 97.8%
similarity. By nucleotide sequence analysis, F105 appears to
be derived from a member of the Vx-11 subgroup gene family.
SQ Sequence 390 bp; 86 A; 115 C; 102 G; 87 T.

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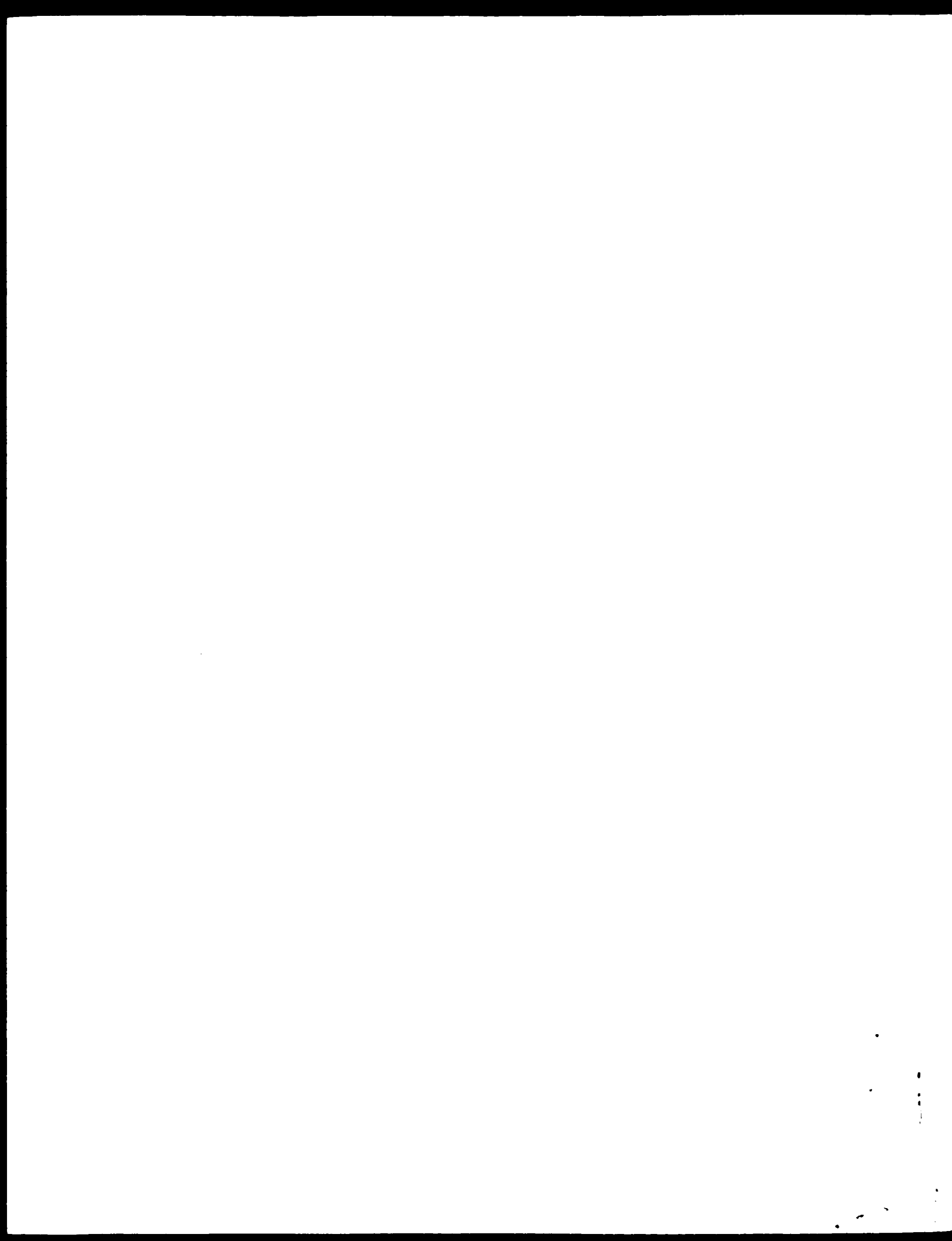
Query Match      77.3%   Score 245:   DR 7:   Length 130:
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CC then fused with mouse myeloma cell line 653 and the resultant clones
 CC were screened using Amb a 1 protein. A single cell subclone AL 16-5.2,
 CC secreting Amb a 1-specific IgG4, kappa antibody was selected. Total
 CC RNA was prep'd. from the AL 16-5.2 cells and first strand cDNA was
 CC pred. using oligo dt primers. When the first strand cDNA was used as
 CC the template, and the 5' and 3' kappa light chain primers (Q66540,
 CC Q66541) were used in PCR and amplified band of the expected size was
 CC noted. The DNA sequence of several subclones contg. this amplified
 CC DNA fragment was determined. The sequence and its deduced AA
 CC sequence are shown in Q66538 and R56286. Comparison of the deduced
 CC AL 16-5.2 L-chain sequence with human V region sequences indicates
 CC that the AL 16-5.2 L-chain is a member of the human VK III subgp.
 SQ Sequence 325 BP: 79 A: 93 C: 79 G: 74 T:

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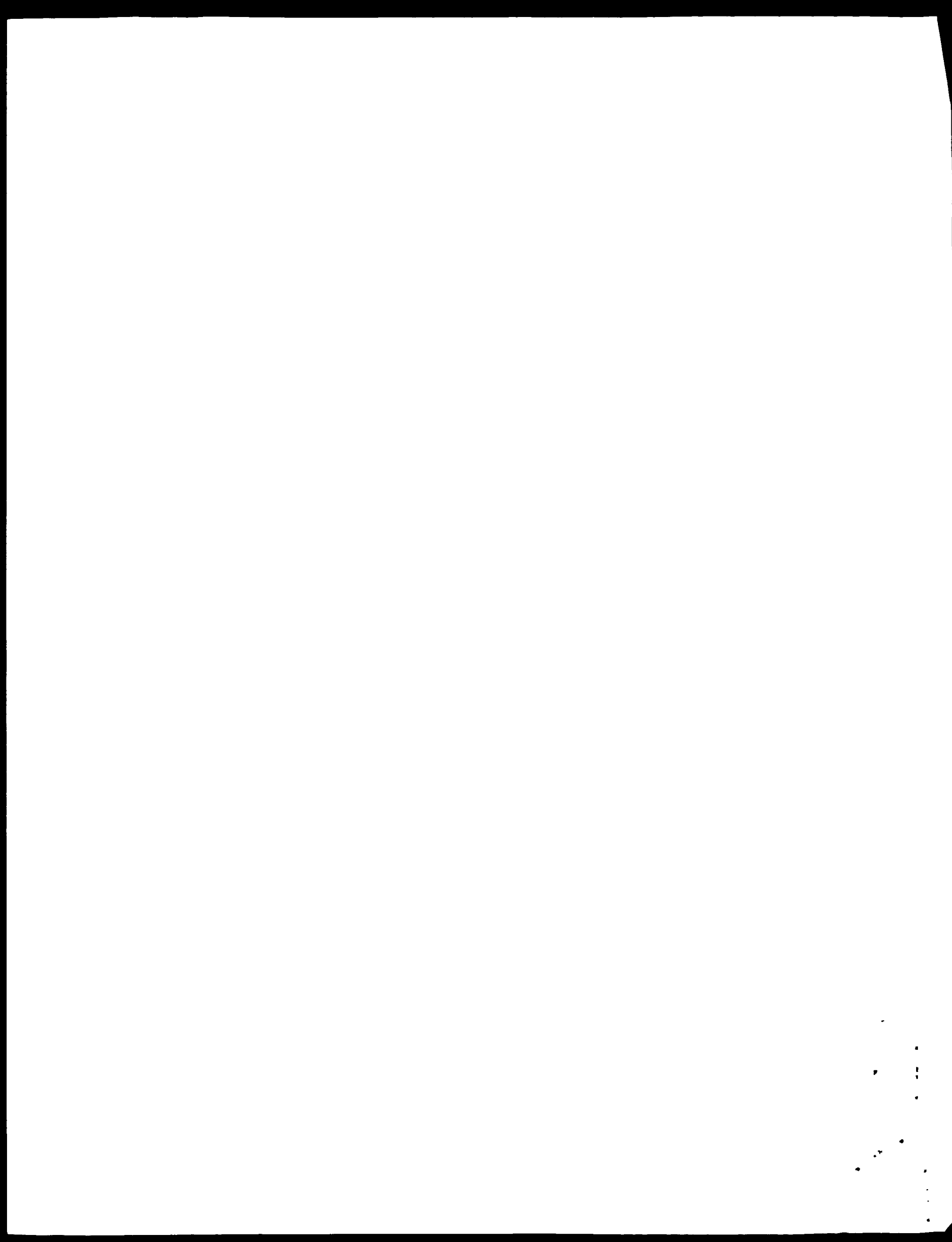
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Thu Feb 26 07:04:57 1998

US-08-844-215-20.rstc

Page 9

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Prod. No.
1	280	88.3	321 91	HSIGVK37F	H.sapiens mRNA for Ig	1.450-226
2	277	87.4	324 98	HMHDPBSAL	Human hepatitis B sur	9.51e-224
3	277	87.4	333 95	HS782772	Human anti-HIV-1 g12	9.51e-224
4	264	83.3	330 93	HS17BVL	H.sapiens immunoglob	1.33e-211
5	264	83.3	332 99	HUMICKAJ	Human Ig active kappa	1.33e-211
6	264	83.3	345 93	HSIM005	H.sapiens mRNA for ka	1.33e-211
7	263	83.0	324 99	HMI-GLVAF	Human clone SpA31-VL	1.14e-210
8	263	83.0	349 98	HMGILIB	Human (clone 1.1) mR	1.14e-210
9	262	82.6	324 91	HSIGVK3C	H.sapiens mRNA for Ig	9.79e-210
10	262	82.6	402 99	HUMICKAI	Human Ig active kappa	9.79e-210
11	262	82.6	402 91	HSIGKVAH	Human mRNA for Ig ka	9.79e-210
12	261	82.3	402 91	HSIGKVIC	Human mRNA for Ig ka	8.19e-209
13	260	82.0	324 95	HS75682	Human rearranged IgM	7.19e-208
14	260	82.0	329 91	HSIGRHE19	H.sapiens (RPMFICK) m	7.19e-208
15	260	82.0	447 99	HMI-GLHHA	Human Ig rearranged	7.19e-208
16	259	81.7	312 91	HSIGRHE18	H.sapiens (RPMFICK) m	6.16e-207
17	259	81.7	318 91	HSIGRHE20	H.sapiens (RPMFICK) m	6.16e-207
18	259	81.7	324 9	HSPEGAL	H.sapiens mRNA for Re	6.16e-207
19	259	81.7	324 93	HSPEGAL	H.sapiens mRNA for Re	6.16e-207
20	258	81.4	320 99	HMI-KAP	Human Ig rearranged k	5.28e-206
21	258	81.4	320 99	HUMICKAI	Human Ig rearranged k	5.28e-206
22	258	81.4	320 99	HUMICKAJ	Human Ig rearranged k	5.28e-206
23	258	81.4	324 94	HS03483	Human clone 37S4 Ig k	5.28e-206
24	258	81.4	324 91	HSIGVLTID	H.sapiens mRNA for Ig	5.28e-206
25	258	81.4	325 99	HUMAB55	Human immunoglobulin	5.28e-206
26	258	81.4	339 99	HSABH1V7	H.sapiens mRNA for ka	5.28e-206
27	258	81.4	364 99	HUMICKAJ	Human Ig rearranged k	5.28e-206
28	258	81.4	387 90	HS0345L	H.sapiens mRNA for an	5.28e-206
29	258	81.4	429 91	HSIGK3S4	H.sapiens rearranged	5.28e-206
30	257	81.1	374 98	HUMFRRP	Homo sapiens mRNA fra	4.52e-205
31	256	80.8	318 99	HUMICKVY2	Human antiplatelet im	3.87e-204
32	256	80.8	324 99	HUMILH1PA	Homo sapiens immuno	3.87e-204
33	256	80.8	390 99	HUMIGHJ3	Human Ig rearranged g	3.87e-204
34	255	80.4	324 99	HUMIKTV3	Homo sapiens Ig kappa	3.87e-204
35	255	80.4	379 92	HSFF1223	H.sapiens mRNA for im	3.87e-204
36	254	80.1	339 99	HUMICKAJ	Homo sapiens (clone S	2.83e-202
37	254	80.1	339 99	HUMICKAJ	Human Ig active kappa	2.83e-202
38	254	80.1	387 97	HUMICKAJ	Human anti-HIV-1 g12	2.83e-202
39	254	80.1	878 99	HUMICKAJ	Human active Igk cha	2.83e-202
40	254	79.8	311 99	HUMICKAJ	Human Ig active kappa	2.83e-202
41	252	79.5	360 99	HUMICKAJ	Homo sapiens (clone 1	2.83e-202
42	252	79.5	324 94	HS03482	Human clone 38S1 Ig k	2.83e-202
43	252	79.5	327 95	HS274567	H.sapiens mRNA for im	2.83e-202
44	252	79.5	333 91	HSIGK28S1	H.sapiens rearranged	2.83e-202
45	252	79.5	339 95	HS034771	Human anti-HIV-1 g12	2.83e-202

ALIGNMENTS

RESULT	1	HSIGVK37F	221 bp	RNA	3'-MAK-1995
LOCUS		H.sapiens mRNA for Ig kappa light chain variable region (V-J).			
DEFINITION		subgroup III (clone 7F).			
ACCESSION		X73858			
NID		g514431			
KEYWORDS		autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup III; Ig variable region; immunoglobulin.			
SOURCE		human.			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
AUTHORS		1 (bases 1 to 321) Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B., Colls,J.C., Peeg,C.A.S., Pees-Smith,B. and Burton,D.K.			
TITLE		Probing the human anti-thyroid peroxidase repertoire of a Hashimoto's thyroiditis patient using combinatorial phage display.			

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4	264	83.3	330 93	HS17BVL	H.sapiens immunoglob	1.33e-211
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6	264	83.3	345 93	HSIM005	H.sapiens mRNA for ka	1.33e-211
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8	263	83.0	349 98	HMGILIB	Human (clone 1.1) mR	1.14e-210
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29	258	81.4	429 91	HSIGK3S4	H.sapiens rearranged	5.28e-206
30	257	81.1	374 98	HUMFRRP	Homo sapiens mRNA fra	4.52e-205
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32	256	80.8	324 99	HUMILH1PA	Homo sapiens immuno	3.87e-204
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34	255	80.4	324 99	HUMIKTV3	Homo sapiens Ig kappa	3.87e-204
35	255	80.4	379 92	HSFF1223	H.sapiens mRNA for im	3.87e-204
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37	254	80.1	339 99	HUMICKAJ	Human Ig active kappa	2.83e-202
38	254	80.1	387 97	HUMICKAJ	Human anti-HIV-1 g12	2.83e-202
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40	254	79.8	311 99	HUMICKAJ	Human Ig active kappa	2.83e-202
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43	252	79.5	327 95	HS274567	H.sapiens mRNA for im	2.83e-202
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RESULT	1	HSIGVK37F	221 bp	RNA	3'-MAK-1995
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NID		g514431			
KEYWORDS		autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup III; Ig variable region; immunoglobulin.			
SOURCE		human.			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
AUTHORS		1 (bases 1 to 321) Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B., Colls,J.C., Peeg,C.A.S., Pees-Smith,B. and Burton,D.K.			
TITLE		Probing the human anti-thyroid peroxidase repertoire of a Hashimoto's thyroiditis patient using combinatorial phage display.			

libraries
 Unpublished
 2 (bases 1 to 321)
 Hexham, J.
 Direct Submission
 Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of
 Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western
 Bank, Sheffield S10 2UH, UK
 3 (bases 1 to 321)
 Hexham, J. M., Furmaniak, J., Pegg, C., Burton, D. P. and Smith, R. P.
 Cloning of a human autoimmune response: preparation and sequencing
 of a human anti-thyroglobulin autoantibody using a combinatorial
 approach
 Autoimmunity 12 (2), 135-141 (1992)
 92314301
 4 (bases 1 to 321)
 Hexham, J. M., Partridge, L. J., Furmaniak, J., Petersen, V. B.,
 Colls, J. C., Pegg, C., Rees, Smith, R. and Burton, D. P.
 Cloning and characterisation of TPO autoantibodies using
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 Thornton, G. B.
 Human combinatorial antibody libraries to hepatitis B surface
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 Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179 (1992)
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 U82772
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 Eukaryotes; mitochondria eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 333)
 Ditzel, H. J., Parren, P. W. H. I., Binley, J. M., Sodroski, J., Moore, J. P.,

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 clone HSSIM005).

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 NID q1296671
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 immunoglobulin light chain; joining region; variable region.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 345)
 AUTHORS Barington,T., Hougs,L., Juul,L., Madsen,H.O., Ryder,L.P.,
 Heilmann,C. and Sveigaard,A.

TITLE The progeny of a single virgin B cell predominates the human recall
 B-cell response to the capsular polysaccharide of Haemophilus

influenzae type b

Unpublished

2 (bases 1 to 345)

Barington,T

Direct Submission

Submitted (01-DEC-1995) Torben Barington, Tissue Typing Laboratory

7631, Pigshospital, National University Hospital, Tagensvej 20,

DK-2200 Copenhagen N, DENMARK

FEATURES

Location/Qualifiers

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/chromosome="2"

/rearranged

1..324

/gene="V-kappa-A27 and J-kappa-4"

V_region

/note="variable region and joining region"
 /product="immunoglobulin kappa light chain"
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/gene="V-kappa-A27 and J-kappa-4"

325..>345

/note="constant region"

BASE COUNT 77 a 96 c 95 g 77 t

ORIGIN

Query Match 83.3% Score 264; DB 99; Length 345.

Best Local Similarity 92.8% Pred. No. 1.33e-211;
 Matches 285; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Db 13 acgagctccaggacacccctgtttgtctccagggaagaagccaccctctctcgcagg 72
 QY 10 AGCAGCTCCAGGACACCCCTGTCTTGTCTCCAGGGAAGAAGACCCCTCTCTCAGAG 69
 Db 73 gccagtcagagtgtaacacagctacttagctgctaccgacagaacacctgaccagct 132
 QY 70 GCTCAGAGTGTACACCAATATTATATATATATATATATATATATATATATATAT 129
 Db 133 caggctctctcatgtatgatacagcagggccacctgggcatccacagacaggttcagg 192
 QY 140 CCGAGGCTCTCATTTATGATGATCAGCAGGAGGCTGCTGCTGCTGCTGCTGCTG 189
 Db 193 cactgggtctgggacagactctcaactcagcagagagagagagagagagagatttgc 252
 QY 190 GGCAGTGGGTCTGGACAGAGACTTCACTCTCAGAGATCAGCAGGAGGAGGAGGAG 249
 Db 253 gcagtcattactctcagcagtagtgtagctacactacgtctcggccaaaggagcaggtg 312
 QY 250 GCAGTGTATTACTCTCAAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 309
 Db 313 gagatca 319
 QY 310 GAAATCA 316

RESULT 7 HUMIGLVAE 324 bp mpna PRI 07-DEC-1994
 LOCUS Human clone SP3-16VL immunoglobulin light chain mRNA V-J region;
 partial cds.

ACCESSION U19910
 NID g348211
 KEYWORDS immunoglobulin light chain; variable region.
 SOURCE Homo sapiens cDNA to mRNA.
 ORGANISM Homo sapiens

Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 324)
 AUTHORS Sasano,M., Burton,R.P. and Silverman,G.J.

TITLE Molecular selection of human antibodies with an unconventional
 bacterial B cell antigen

J. Immunol. 151 (10), 5822-5829 (1993)

94044806

2 (bases 1 to 324)

Silverman,G.J.

Direct Submission

Submitted (02-AUG-1993) G.J. Silverman, Sam and Rose Stein

Institute for Research on Aging, University of California at San

Diego, La Jolla, CA 92093, USA

FEATURES

Location/Qualifiers

1..324

/organism="Homo sapiens"

/strain="Caucasian"

/cell_type="lymphocyte"

/dev_stage="adult"

/sex="male"

/tissue_type="peripheral blood"

/tissue_lib="pComb3-JT0 (M13 phagemid vector)"

/clone="SpA3-16VL"

1..>324

/note="binds Staphylococcal protein A (SpA)"

CDS

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KRLVYGTSSPATGIP:FFSSSSSGTINFLITSLRLEPEFPAVYQYVGSQWFSGGI
VVELKR"
BASE COUNT      71 a   97 c   90 g   56 t
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Best Local Similarity 91.2%; Pred. No. 1,14e-210;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 4 gccgaactcaacagctctccaggaacccctgtctttgtctccaggggaaagaccaccc 63
QY 1 GCGGAGCTCAACGCA:PTTCAAGCA:GCTGTCTTTTGTCTCAAGSSAAAGAGCCACCC 60
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Db 64 tctcgcagggccagctccagctgttagcagggccctacttagctgtgacccagcagaacct 123
QY 1 GCGGAGCTCAACGCA:PTTCAAGCA:GCTGTCTTTTGTCTCAAGSSAAAGAGCCACCC 120
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Db 124 gccgaactcaacagctctctctctatgtgacatccagcagggccactggcatcccgag 183
QY 121 GCGGAGCTCTCCAGGCTCTTCAITTTATGATCATCCAGCAGGGCCACTGGCATCCCGAG 180
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Db 184 aggttcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 243
QY 181 AGGTCAGTGGCAGTGGGCTCTGGGACAGACTTCATCTTCAGCATCAGCAGATTCGAGCCT 240
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Db 244 gaagattttcagctactactctcagcagtcagtcagtcagtcagtcagtcagtcagtcag 303
QY 241 GAAGATTTCAGCTATTACTGTCTAGAGTAA:ACCTTCACATCTTGGCCAGGG 300
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Db 304 accaagtcgaactcaaa 321
QY 301 ACCAAGTGGAAATCAAA 318
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RESULT 8 HUMG1118 648 bp mRNA PRI 22-JUL-1993
LOCUS Human (clone 1.L) mRNA sequence.
ACCESSION L22157
NID 9347321
KEYWORDS Homo sapiens adult blood cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata,
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 648)
AUTHORS Barbas,C.F.III., Kang,A.S., Lerner,R.A. and Benkovic,S.J.
TITLE Assembly of combinatorial antibody libraries on phage surfaces: The
gene III site
JOURNAL Proc. Natl Acad Sci U S A 88, 7078-7082 (1991)
MEDLINE 9137609
FEATURES Location/Qualifiers
source
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/cell_type="lymphocyte"
/dev_stage="adult"
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BASE COUNT 159 a 189 c 171 g 129 t
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Best Local Similarity 91.2%; Pred. No. 1,14e-210;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0.

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QY 1 GCGGAGCTCAACGCA:PTTCAAGCA:GCTGTCTTTTGTCTCAAGSSAAAGAGCCACCC 60
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Db 63 tctcgcagggccagctccagctgttagcagggccctacttagctgtgacccagcagaacct 122
QY 1 GCGGAGCTCAACGCA:PTTCAAGCA:GCTGTCTTTTGTCTCAAGSSAAAGAGCCACCC 120
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QY 61 TCTCTCAGGGGCGACGACAGCTCTTAGCTAG:AAATATTATTA:NTGATCAACAGAAACCT 120
DB 123 gccgaactcaacagctctctctctatgtgacatccagcagggccactggcatcccgag 182
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QY 121 GCGGAGCTCTCCAGGCTCTTCAITTTATGATCATCCAGCAGGGCCACTGGCATCCCGAG 180
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Db 183 aggttcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 242
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QY 181 AGGTCAGTGGCAGTGGGCTCTGGGACAGACTTCATCTTCAGCATCAGCAGATTCGAGCCT 240
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Db 243 gaagattttcagctactactctcagcagtcagtcagtcagtcagtcagtcagtcagtcag 302
QY 241 GAAGATTTCAGCTATTACTGTCTAGAGTAA:ACCTTCACATCTTGGCCAGGG 300
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Db 303 accaagtcgaactcaaa 320
QY 301 ACCAAGTGGAAATCAAA 318
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RESULT 9 HSTGVK3C3 324 bp RNA PRI 30-MAR-1995
LOCUS H.sapiens mRNA for Ig kappa light chain variable region
DEFINITION (V-J).subgroup III (clone C3).
ACCESSION X73863
NID g516187
KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup III;
Ig variable region; immunoglobulin.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B.,
Colls,J.C., Pegg,C.A.S., Pees-Smith,B. and Burton,D.R.,
TITLE Probing the human anti-thyroid peroxidase repertoire of a
Hashimoto's thyroiditis patient using combinatorial phage display
libraries
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 324)
AUTHORS Hexham,J.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of
Mol Biology and Biotechnology, P. O. Box 594, Firth Court, Western
Bank, Sheffield S10 2UH, UK
REFERENCE 3 (bases 1 to 324)
AUTHORS Hexham,J.M., Furmaniak,J., Pegg,C., Burton,D.P. and Smith,B.R.
TITLE Cloning of a human autoimmune response: preparation and sequencing
of a human anti-thyroglobulin autoantibody using a combinatorial
approach
JOURNAL Autoimmunity 12 (2), 135-141 (1992)
MEDLINE 92314301
REFERENCE 4 (bases 1 to 324)
AUTHORS Hexham,J.M., Partridge,L.J., Furmaniak,J., Petersen,V.B.,
Colls,J.C., Pegg,C., Pees-Smith,B. and Burton,D.R.
TITLE Cloning and characterisation of IPO autoantibodies using
combinatorial phage display libraries
JOURNAL Autoimmunity 17 (3), 167-179 (1994)
MEDLINE 95035699
FEATURES Location/Qualifiers
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Matches 297; Conservative 0; Mismatches 18; Indels 3; Gaps 1.

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QY 4 GAGCTCAGCAGCTCTCCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63
Db 61 tccagggccagctcagagtgcttagcagcagctactagctctgaccagcagaaaacctggc 120
QY 64 TCCAGGGCCAGCTCAGAGTCTTAAGTACCAAAATACCTTAGCTAGTACCAAGAAACCTTGGC 123
Db 121 cagctctccagcagctctctctctctctctctcagcagcagcagcagcagcagcagcag 180
QY 124 CAGGCTCCCCAGGCTCTTCATTTATGATGATCCAGCAGGCGCACTGGCATCCCGACAGAGG 183
Db 181 ttcaaggcagctgggtctgggacagctctctctctcaccatcagcagcagcagcagcagc 240
QY 184 TTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCTCAGCATCAGCAGATTGGAGCCTGAA 243
Db 241 gatttgcaagtattactcgtcagcagctatgtagctcacccttgagcgttcggccaagg 300
QY 244 GATTTTGCAGTGTATTACTGTGTCAGCAGTATGSA---CACTTCGACACTTCGCGCCAGGG 300
Db 301 tccaagggtgaaatcaaa 318
QY 301 ACCAAGGTGGAATCAAA 318

RESULT 10 HUMIGKAI 402 bp mRNA PRI 15-DEC-1989
LOCUS Human Ig active kappa chain mRNA V-region (V-J1-C), clone NOV.
DEFINITION M27025
ACCESSION g185845
NID C-region; V-region; immunoglobulin light chain;
KEYWORDS immunoglobulin-kappa; processed gene.
SOURCE Human salivary gland B lymphocyte cDNA to mRNA, clone NOV.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 402)
AUTHORS Kipps T.J., Tomhave E., Chen P.P. and Fox P.J.
TITLE Molecular characterization of a major autoantibody-associated
cross-reactive idiotype in Sjogren's syndrome
JOURNAL J. Immunol. 142, 4261-4268 (1989)
MEDLINE 89256674
COMMENT Draft entry and printed copy of sequence kindly submitted by
T.J.Kipps, 16-AUG-1989.
FEATURES
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1..402
/organism="Homo sapiens"
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CDS 1..>402
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Best Local Similarity 94.2%  Pred. No. 9,790-210;
Matches 294; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

Db 73 acgagctctccagcagcagctgtgtctgtctgtctgtctgtctgtctgtctgtctgtct 132

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Matches	293:	Conservative	0:	Mismatches	16:	Indels	3:	Gaps	2:
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QY	10	AGGACATCTTCAGGACACCTGCTTGGTTCCTCAAGGAAAACATCAATCTCTGACAGG	69						
Db	64	ggcagtcagagtggttagcagcagctacttagcctgggtaccagcagaaacctggccagcgt	123						
QY	70	GGCAATCAGAGTCTTAGTAGCAACAAACATTAAGCTNAGTATCAATAGAAAGCTGGGTAGGCT	129						
Db	124	ccagcgtctctcatctatgggtgcatccagcagggccactggcactccccagcagcaggttcagtt	183						
QY	130	CCGACGGCTCTTCATTATTATGATGCTGCAGAGAGAGGCTACTGGCATTCCTCAGACAGTTTACG	189						
Db	184	ggcagtcgggtctggacacagacttcactctccaccatcagcagactggagcctggaagatttt	243						
QY	190	GGCAGTGGGTCTGGCAGCAGACTTCACCTCTCAGCATCAGCAGATTGGAGCCTGAGAGATTIT	249						
Db	244	gcagctattactctgcacacgaatctggtaactcaactcagcaggttcggcccaaggagcacaag	303						
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QY	307	GTGGAATCAAA	318						

RESULT	15				
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DEFINITION	Human Ig rearranged gamma-chain mRNA V-region, partial cds.				
ACCESSION	L03162				
NID	9185397				
KEYWORDS	V-region; immunoglobulin gamma-chain; immunoglobulin heavy chain; processed gene				
SOURCE	homo sapiens (tissue library: BMHIV) adult female cDNA to mRNA.				
ORGANISM	homo sapiens				
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 447)				
AUTHORS	Collet,T A., Roben,P., O'Kennedy,P., Barbas,C F III., Burton,D.R., and Lerner,R.A.				
TITLE	A binary plasmid system for shuffling combinatorial antibody libraries				
JOURNAL	Proc. Natl. Acad. Sci. U S A. 89 (21). 10026-10030 (1992)				
MEDLINE	93066172				
FEATURES	Location/Qualifiers				
Source	1..447				

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FEATURES
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Location/Qualifiers
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/dev_stage="adult"
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/map="14q32.33"
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/gene="IGHV@"
1..>447
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VEIKPTVAASVPIFPDSQELKSGTASVCLINNEYPEAKVQWFW"
102 a 126 c 117 g 102 t
BASE COUNT

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VEINPILAP:VEITPPELLE:LA
CUT 126 117 103

ORIGIN

Query Match 82.0% Score 260 DB 99 Length 447
Best Local Similarity 93.1% Pred. NO. 7.19e-208
Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Db 1 gagctcaagcagctccaggggacccctgtctgtctctccaggggaaaagaccacccctctcc 60
QY 4 GAGCTCAAGCTACAGGACCCCTGTCTGTCTCTCCAGGGGAAAAGACCCCTCTCC 63

Db 61 tgcaggggcagctcagagtggtattacagcaactacttagcctggtaccagcagaaaacctggc 120
QY 64 TGCAGGGGCAGCTCAGAGTGTATTACAGCAAAATACCTAGTACCAACAGAAACCTGGC 123

Db 121 caagctccagagctcctcatctatgtatgtatccaaagggccactgacatcccaagacagg 180
QY 124 CAGGCTCCAGAGCTCTCTATTTATGATGTCATCCAGCAGGGCCACTGGCATCCACAGCAGG 183

Db 181 ttcaatggcagtggtctgggacagacttcactctcaccatcagcaactgagaccctgaa 240
QY 184 TTCAGTGGCAGTGGGTCTGGGACACACTTCACTCTCAACATCAGCAATGAGCCCTGAA 243

Db 241 gattttgcagtgattctcctgtcagcagtgatggtacctcaccgtgagcgttcggccaaagg 300
QY 244 GATTITGCAGCTGATTACTGTGACAGTATGGAAC---ACCTGCACCTTGGGCCAGGGG 300

Db 301 accaagtggaatacaaa 318
QY 301 ACCAGGTGGAAATCAAA 318

Search completed: Tue Feb 24 09:17:42 1998
Job time : 436 secs.

WATERMAN

Release 2.1D John F. Collins, BioComputing Research Unit,
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MPsrch_hn n.a. - a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 09:05:21 1998: MasPar time 118.99 seconds
Tabular output not generated. 753,699 Million cell updates/sec

Title: >US-08-844-215-20
Description: (1-318) from US08844215.seq
Perfect Score: 317
N.A. Sequence: 1 GAGGAGTTCACAGAGTTCG
Comp: CGGCTGAGTTCACAGAGTTCG

Scoring table: TABLE default
Gap f
Nmatch STD : Dbase Q: Query Q
Searched: 397346 seqs. 141010104 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-C
1: EST197 2: EST198 3: EST199 4: EST200 5: EST201 6: EST202
7: EST203 8: EST204 9: EST205 10: EST206 11: EST207 12: EST208
13: EST209 14: EST210 15: EST211 16: EST212 17: EST213
18: EST214 19: EST215 20: EST216 21: EST217 22: EST218
23: EST219 24: EST220 25: EST221 26: EST222 27: EST223
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114: EST310 115: EST311 116: EST312 117: EST313 118: EST314
119: EST315

Statistics: Mean 9 746: Variance 1 743: scale 5 593

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description	Pred. No.
1	237	74.8	413	27	AA301347	EST14279 Testis tumor
2	229	72.3	352	27	AA301347	EST14279 Testis tumor
3	218	68.9	335	33	AA318377	EST20620 Spleen I Hom
4	217	58.5	345	39	AA335086	EST13457 Esophagus tu
5	215	47.8	357	25	AA341447	EST17140 T-cell lymph
6	214	57.5	382	25	AA255794	EST10087 Pancreas tu
7	199	62.8	334	37	AA327254	EST10547 Colon I Hom
8	195	61.5	303	26	AA300891	EST13648 Testis tumor
9	195	61.5	303	26	AA300891	EST13648 Testis tumor
10	195	61.5	303	26	AA300891	EST13648 Testis tumor
11	184	57.7	301	58	AA377235	EST14647 Small intest
12	180	56.8	282	26	AA300491	EST13404 Testis tumor
13	176	55.5	292	24	AA255508	EST100751 Pancreas tu
14	176	55.5	292	24	AA255508	EST100751 Pancreas tu
15	167	52.7	289	25	AA245841	EST14275 Testis tumor
16	161	50.8	288	55	AA366827	EST101850 Pancreas tu
17	155	48.9	282	37	AA327542	EST17860 Pancreas tum
18	136	42.9	329	24	AA255311	EST160471 Pancreas tu
19	132	41.6	370	24	AA295093	EST103400 Pancreas tu
20	132	41.6	403	73	AA345486	EST151505 Gall bladder
21	130	41.0	279	24	AA244843	EST103059 Pancreas tu
22	138	40.4	338	33	AA318524	EST10808 Spleen I Hom
23	128	40.4	400	116	AA456778	EST22111 rl Soares ova
24	127	40.1	253	25	AA255941	EST101155 Thymus t
25	127	40.1	269	24	AA294819	EST100059 Pancreas tu
26	127	40.1	291	55	AA366485	EST177625 Pancreas tum
27	125	39.4	323	37	AA327357	EST30702 Colon I Homo
28	123	38.8	308	55	AA335692	EST177429 Pancreas tum
29	123	38.8	345	26	AA300582	EST113427 Testis tumor
30	121	38.2	363	55	AA367405	EST17811 Pancreas tum
31	110	34.7	281	35	AA321455	EST23932 Bone marrow
32	110	34.7	349	59	AA379044	EST19999 Skin tumor
33	108	34.1	205	52	AA360654	EST169843 T-cell lymph
34	105	33.1	303	52	AA360281	EST169401 Lymph node
35	96	30.3	196	27	AA311279	EST114202 Testis tumor
36	96	30.3	402	90	CG2426	HMG50012003 Human
37	96	30.3	405	52	AA360223	EST16241 Lymph node
38	93	29.3	160	116	AA455218	EST17855 rl Soares ova
39	93	29.3	203	25	AA255622	EST100796 Pancreas tu
40	93	29.3	283	53	AA361578	EST170983 T-cell lymph
41	92	29.0	293	37	AA337497	EST13944 Colon I Homo
42	86	27.1	398	84	AA433447	EST08003 rl Soares mou
43	84	26.5	338	62	AA388214	EST17387 Thymus I Ho
44	82	25.9	145	22	AA245674	EST11150 Thymus tumor
45	80	25.2	249	86	AA430449	EST20111 rl Soares ova

ALIGNMENTS

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LOCUS AA301347 413 bp mRNA EST 18 APR 1997
DEFINITION EST14279 Testis tumor Homo sapiens cDNA 5' end similar to similar
to human alpha 1B kappa light chain, V region (AF047079).
ACCESSION AA301347
NID G1953680
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Faldut, R.A.,
Buit, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, W.L., C.
Clayton, R.A., Gline, T.P., Cotton, M.D., Earle-Hughes, J., Fink, L.D.,
Fitzgerald, L.M., Fritch, W.M., Fritchman, T., Gachazan, N.S.,
Glodek, A., Gnehm, C.I., Hanna, M.C., Hedblom, E., Hinkle, P.S., J.


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Db 307 ttgcgaattactactgtcaacagagttaca 337
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RESULT 3 AA318377 335 bp mRNA EST 19-APR-1997
LOCUS EST06620 Spleen 1 Homo sapiens cDNA 5' end similar to
DEFINITION immunoglobulin kappa light chain, V region, anti-thyroglobulin
(GR-X79786)
ACCESSION AA318377
NID d1970863
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 335)
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geohagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.M.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudex, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y.,
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Dimke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S., Olsen, H.,
Paymond, L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Dillon, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (5547 Suppl), 3-174 (1995)
96026280
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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Best Local Similarity 90.6% Pred No 0.00e+00;
Matches 241; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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99. The hundredth column is labeled "SOURCE".	

TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence					
JOURNAL MEDLINE COMMENT	Nature 377 (6547 Suppl), 3-174 (1995) 95026280					
Contact:	Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi.html) Seq primer: M13 Reverse.					
FEATURES	Location/Qualifiers					
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ORIGIN						
Query Match	62.8%; Score 199; DB 37; Length 334;					
Best Local Similarity	88.9%; Pred. No. 0.00e+00;					
Matches	231; Conservative 0; Mismatches 28; Indels 1; Gaps 1;					
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QY	5 AGCTCAACATCTCCATGCGTCCTTCTGTATTGGTAGAGAGAGAGAGAGAGAGAG 64					
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Db	195 ccctaagcctcgtcatctatctcgctccagtttgcaaatggagggtcccacaaattca 254					
QY	125 CCGCTAAGTGCTTTGATCTTATGCTGCATCTACATTTTGAAGATGAGATGAGAGGTTTCA 184					
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LOCUS	AA300788 303 bp mRNA EST 18-APR-1997					
DEFINITION	EST13648 Testis tumor Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region.					
ACCESSION	AA300788					
NID	g1953120					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrates; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
AUTHORS	1 (bases 1 to 303)					
ADDITIONAL	Adams M.D., Kerlavage A.P., Fleischmann P.D., Fuldner R.A., White O.J., Sutton G., Blake J.A., Brandon P.C., Man-wai C., Clayton P.A., Cline T.B., Cotton M.D., Earle-Hughes N.S., Fitzgerald L.M., Fitchum W.M., Fritchman J.E., Geoghagan N.S., Glodok A., Gnehm C.I., Hanna M.C., Hedblom E., Hinkle P.S., Kelley J.M., Kelley J.C., Li L., Li Y., Marmaros S.M., Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley P., Small K.V., Spriggs T.A., Utterback T.R., Waldman J.F., Wiley B., Bednarek D., Feng D.-F., Ferrie A., Fischer J., Hastings G.A., Dinke D., Peng D., Greene J.M., Gruber J., Hudson P., Kim A.K., He W.W., Hu J.S., Kunsch C., Hungjun J., Li L.H., Weissner P.S., Olsen H., Raymond L., Wei Y.F., Wind T., Xu C., Yu G.L., Pupen S.M., Dillison P.J., Fannon M.P., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M., and Ventor J.C.					



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MPsrch_nno n.a. - n.a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 14:41:59 1998 Maspar time 19.80 Seconds
Tabular output not generated. 738,645 Million cell updates/sec
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Scoring table: TABLE default
Gap 5
Nmatch STD : Dbase 0: Query 0
Searched: 87531 seqs, 2294621 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: n-issued
1-back 2-51 3-52 4-53 5-54 6-55 7-56 8-PT90 9-PT91
10-PT92 11-PT93 12-PT94 13-PT95 14-PT96
Statistics: Mean 7.594: Variance 4.023: scale 1.888
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES						
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40 155 48.9 1952 7 US-08-401- Sequence 16, Application 8, 110-100
41 150 47.3 729 6 US-08-236- Sequence 3, Application 5, 590-96
42 147 46.4 321 12 PT-US94-0 Sequence 7, Application 1, 450-93
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ALIGNMENTS

RESULT 1
ID US-08-300-386A-62 STANDARD: DNA: UNC: 280 BP.
AC xxxxxx
DI 01-JAN-1900
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CC Sequence 62, Application US/2830386A
CC Patent No. 5667988
CC GENERAL INFORMATION:
CC APPLICANT: Barbas, Carlos F. III
CC APPLICANT: Burton, Dennis R.
CC APPLICANT: Lerner, Richard A.
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIPESAL OR RANDOMIZED IMMUNOGENIC LIGANDS
CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10550 N. Torrey Pines Road, TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patented Release # 1.1, Version # 1.15
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/300,386A
CC FILING DATE: 02-SEP-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/825,623
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993

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CC ORGANISM: Homo sapiens
CC CELL TYPE: Hybridoma
CC CELL LINE: ZM1-2
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..384
SQ Sequence 384 BP: 83 A: 108 C: 100 G: 93 T: 0 other:
    Query Match 72.2%, Score 229, DB 7, Length 384;
    Best Local Similarity 86.3%, Pred. No. 3, 16e-158;
    Matches 271; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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Db 128 GTCGGGCGAGTCAGGTATTAGCAGTTGGTTAGCCCTGGTATCAGCAGAAACCCAGGAAAG 187
QY 65 GCGGGGCAAGTCAGAGTATTATAGCAAACTTAAATTCGTATCAGCAAGAACCCAGGAGAG 124
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QY 245 TTGCAACTTACTATTGTCAACAGGCTGACAGTCTCCCTTTTACTTTTGGCGGAGGAGCA 304
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DE 01-JAN-1900
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CC Patent No. 5661016
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/940,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:

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CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO. 184:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 847 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: Join(226, 279, 405, 700)
CC Sequence 847 BP: 200 A: 231 C: 203 G: 213 T: 0 other:
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QY 245 TTGCAACTTACTATTGTCAACAG 267

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DE 01-JAN-1900
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CC Sequence 1, Application US/08217918
CC Patent No. 5506132
CC GENERAL INFORMATION:
CC APPLICANT: LAKE, PHILIP
CC APPLICANT: OSTBERG, LARS
CC TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
CC TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/217,918

```

CC FILING DATE: 24-MAR-1994
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 387 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..387
CC Sequence 387 BP: 97 A: 107 C: 94 G: 90 T: 96

Query Match 65.7%; Score 207; DP 6; Length 387;
Best Local Similarity 82.8%; Pred. No. 8.93e-141.

[illegible]

RESULT	7
ID	PCT-US92-09487-74 STANDARD; DNA; UNC; 321 BF.

AXXXXX
01-JAN-1900
Sequence 74, Application PC/TUS9209487.
Sequence 74, Application PC/TUS9209487.
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Compr
TITLE OF INVENTION: Preparation and

CC NUMBER OF SEQUENCES: 101
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O
CC ADDRESSEE: Ricknell
CC STREET: Two First Natl
CC STREET
CC CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPIER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patsoft Release 1.0, Version 1.25
CURRENT APPLICATION DATA: PCT/US92/00497
APPLICATION NUMBER: PCT/US92/00497
FILING DATE: 19921104
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35402
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: NUCLEIC ACID
STRETCH: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
Sequence 321 bp: 89 A: 73 C: 77 G: 82 T: 0 other:

Query Match 61.58; Score 195; DB 10; Length 321;
Best Local Similarity 89.98; Pred. No. 2.78e-131;
Matches 254; Conservative 0; Mismatches 60; Indels 0

[illegible]

```

RESULT      8
ID          US-08-425-236-72 STANDARD: DNA: UNC: 211 BP.
AC          xxxxxx
DI          UL-JAN-1900
DE          Sequence 72, Application US/09425236.
DE          Sequence 72, Application US/09425236.
CC          Patent No. 5621083
CC          GENERAL INFORMATION:
CC          APPLICANT: Better. Marc D.

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[illegible]

RESULT

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QY 302 CCAAGTGGAGTCAAA 318
|||||
RESULT 3
LOCUS p29232 501 bp mRNA EST 25-APR-1995
DEFINITION YH5TERA v1 Homo sapiens cDNA clone 133862 c1 similar to p29232
IG KAPPA CHAIN V-1 REGION (HUMAN);
ACCESSION R2232
NID g784367
KEYWORDS EST;
SOURCE human clone-133862 library-Soares placenta Nb2HP vector-pT7T3D
(Pharmacia) with a modified polylinker host-pH10B (ampicillin
resistant) primer-M13R1 Psic1-Not I Rsi12-Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - 3192(37) primer [5].
ACCTGAAGAAATTCGGGCGCAGGAAATTTTTTTTTT 3', double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo.
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS Hillier, L., Clark, N., Dubuque, I., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63104
Tel: 314 285 1800
Fax: 314 285 1810
Email: est@watson.wustl.edu
High quality sequence steps: 282
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Source 1..503
Location/Qualifiers
/organism="Homo sapiens"
/clone="133862"
BASE COUNT 117 a 122 c 133 g 122 t 9 others
ORIGIN
Query Match 55.2%, Score 175, DB 22, Length 503,
Best Local Similarity 86.2%, Pred No. 0.00e+00:
Matches 213: Conservative 0: Mismatches 33: Indels 1: Gaps 1:
Db 5 ungcagacacacattagcagactattaaattgattatcagcaaacacagcagacccc 64
QY 68 GGGCAAGTCACAGATTATTAAGAGAAATTAAATGGATACAGAGAAAGAGAGAGAGCC 127
|||||
Db 65 ctgaactgcgatctattctgcgtcccatcttgcaaaagtggaggtcccccaggttcagt 124
QY 126 GTAAAGTCTGATCTATGCTGATATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
|||||
Db 125 cgaatcgaatcagagacacattcactctcactcactcactcactcactcactcactcact 184
QY 168 ACATGATATGTCACATATATATATATATATATATATATATATATATATATATATAT 247
|||||
Db 165 cgaatcgaatcagagacacattcactcactcactcactcactcactcactcactcact 244
QY 248 CAACTTATATGTCACATATATATATATATATATATATATATATATATATATATATAT 306
|||||
Db 245 atgagag 251
|||||

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QY 307 GTGGAAG 313
|||||
RESULT 4
LOCUS T29112 395 bp mRNA EST 06 SEP 1995
DEFINITION EST69384 Homo sapiens cDNA 5' end similar to human ribosomal kappa
18S1 chain V region (H K1204) (H13619).
ACCESSION T29112
NID g611210
KEYWORDS EST;
SOURCE human primer-M13 Reverse library-Human Lymphoid tissue.
ORGANISM Homo sapiens
Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostoma; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 395)
AUTHORS Adams, M. D., Kervatage, A. P., Fleischmann, P. D., Feldner, P. A.,
Bult, C. J., Lee, N., Kinkness, E. F., Weinstock, J. G., Gerbelye, J. D.,
White, C. J., Sutton, G., Blake, J. A., Brand, R. P. C., Chin, M. W.,
Clayton, R. A., Cline, P. T., Cotton, M. D., Earle-Hughes, J., Fine, L. B.,
FitzGerald, L. M., Fitch, W. M., Fritchman, J. B., Goodhead, N. S. M.,
Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, J. P. S.,
Kelley, J. M., Klimek, K. M., Kelley, J. C., Liu, J. T., Marmore, S. M.,
Merrick, J. M., Moreno-Palacios, P. F., McDonald, J. A., Nguyen, D. T.,
Pellegrino, S. M., Phillips, C. A., Poyer, S. E., Scott, J. L.,
Saudok, D. M., Shirley, B., Small, K. V., Spriggs, T. A., Strickland, J. K.,
Weidman, J. F., Willy, Bednarik, D. P., Cao, L., Cepeda, M. A.,
Coleman, T. A., Collins, E. J., Dimke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M.,
Gruber, J., Hudson, P., Kim, A., Kozay, D. L., Kunsch, G., Li, H., Li, H.,
Meissner, P. S., Olsen, H., Paymond, L., Wei, Y. F., Wied, J., Xu, G.,
Yu, G. L., Ruben, S. M., Dillon, P. J., Fannon, M. R., Rosen, C. A.,
Haseitine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)
Other ESTs: EST69383
Contact: Venter, J. C.
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
FEATURES
Source 1..395
Location/Qualifiers
/organism="Homo sapiens"
/clone="133862"
BASE COUNT 87 a 110 c 95 g 96 t 7 others
ORIGIN
Query Match 53.0%, Score 168, DB 58, Length 395,
Best Local Similarity 84.5%, Pred No. 0.00e+00:
Matches 213: Conservative 0: Mismatches 37: Indels 2: Gaps 2:
Db 70 agttgacccagctccacacctcctcctcctcctcctcctcctcctcctcctcctcct 129
QY 5 AGCTCACCCAGTCTCCATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64
|||||
Db 130 gccagggcagtcagacattagcagttatttagccttgatcaccacacacacacacacac 149
QY 65 GCGGCGGGAAGTCAGATATTAGAGAGAACTTAAATGGATACAGAGAGAGAGAGAGAG 124
|||||
Db 190 cccctgaactcctcactcactcactcactcactcactcactcactcactcactcactcact 249
QY 125 CCGCTTAAGTCTGATCTATGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 184
|||||
Db 250 ggggggggggggggggggggggggggggggggggggggggggggggggggggggggggg 409
|||||
QY 185 GTGGCAGTGGATCTGGGACATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 442
|||||

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Ddb	310	ttctgcgactta	321
QY	243	TTTTCGAACCTTA	254

RESULT	5	T27221	288 bp	mRNA	EST	06-SEP-1995
LOCUS		EST13641 Homo sapiens cDNA 5' end similar to immunoglobulin light chain V region, rearranged (HT:3785).				
DEFINITION		T27221				
ACCESSION		a609819				
NID		NTD				
KEYWORDS		EST..				
SOURCE		human primer-M13 Reverse library-Human Testis.				
ORGANISM		Homo sapiens				

Eukaryoteae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata, Vertebrata; Gnathostomata, Osteichthyes, Sarcopterygii, Chonantia; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 288)

Adams M.D., Kerlavage A.P., Fleischmann P.D., Fuldner P.A., Bult C.J., Lee N.C., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Child M.W., Clayton P.A., Cline P.T., Cotton M.D., Earle-Hughes J., Fine L.D., Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodak C.A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr. P.S., Kelley J.M., Klimek K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merriell J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley P., Small K.V., Spriggs T.A., Utterback T.P., Weidman J.F., Li Y., Bednarek D.P., Cao L., Cepeda M.A., Coleman I.A., Collins E.S., Dimke S., Feng F., Ferrie A., Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Messner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C., Yu G.-L., Puken S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M. and Venter J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence Unpublished (1995)
Other ESTs: THC24356
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd. Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tldb.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tldb.tigr.org).

FEATURES	
Source	1..288
	/organism="Homo sapiens"
BASE COUNT	<1> ^288
ORIGIN	65 a 75 c 70 g 67 t 11 others
Query Match:	52.7%, Score 167, DB 58, Length 288,
Best Local Similarity	88.6%; Pred. No. 0.00e+00;
Matches	203; Conservative 0; Mismatches 22; Indels 4; Gaps 4;

Ddb	60	agatgaccagtntccatcgctcctgttgtcatctnttaggcacagagtcacctcaatt	119
QY	5	AGCTCACCGAGTCTCCATCGTGCTCTGTCTGATTGTNGSAGACAGAGTACCATCACT	64
Ddb	120	gccgggcaagtnagacgattagcagctattaanttggtatcacgcagaacaacagggaag	179
QY	65	GCCGGGCAGTCAGAGTATTACGACGAACTTAATTGGTATCAGCAAACACCGGACAG	124
Ddb	180	cccctaagctcctnatctatgctgcgatccagcttgccaagtgggggtcccataoagttc	239
QY	125	CCCCTAAGCTCCTGATCATGCTGATGTCATGCCAGTTTGCAAGTGGGG-TCCCATCAGGTC	183

```

LOCUS       T93178             434 bp     mRNA             EST             22-MAR-1995
DEFINITION  Y93178 r1 Homo sapiens cDNA clone 118692 5' similar to gb:U33034
            IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION   T93178
NID         G725091
KEYWORDS    EST.
SOURCE      human c-one-118692 library-Stratagene lung (#937210)
            vector-pBluescript SK+ host-SUP cells (kanamycin resistant)
            primer-M33P1 Psitel-EcoRI Psitel-XbaI Normal lung tissue from a 72
            year old male. Cloned unidirectionally. Primer: Oligo dT. Average
            insert size: 1.0 kb. Uni-ZAP XR Vector; 5' adaptor sequence:
            5'-GAATTCGGCAGAG-3'; 3' adaptor sequence:
            5'-CTCGAGTGTGTTTTTTTTT-3'.
ORGANISM    Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 434)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,F.,
            Waterston,R., Williamson,A., Wohlmann,P. and Wilson,P.
TITLE       WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson PK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 265
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             source
                     1..434
                     /organism="Homo sapiens"
                     /clone="118692"
BASE COUNT   103 a 107 c 103 g 118 t      3 others
ORIGIN
Query Match      41.3%   Score 131; DR 11; Length 434;
Best Local Similarity 78.9%   Pred. No. 1 260-227;
Matches 191; Conservative 0; Mismatches 49; Indels 2; Gaps 2;
Db 1 actgcccgggca-gtcaagacattagtattttagctgtatcagcaaaaatcaggg 59
QY 61 ACTTGTGGGGTAAATGAGATATAGTGAAGATTAATATGATATAGCAGAAATCAGG 120
Db 60 aaagccctaaagctccctgtatgtgtcattccactttgaacacttgggtcccatcagg 119
QY 121 ACAGTCTTAAGGTCTGTGATGTATGTGATATGATAGTATGATAGTATGATAGT 180
Db 120 ttcaagggcgaatgagatcagcagaaattcactctcaaatcagcagcctcgaactga 179
QY 181 TTAGTGGTATGG-ATCTGGGACAGATTCATCTGTCATCATCATCATCATCATCAT 239
Db 180 aaactatgcaacctattactcagcagcgttcattagctctccctcgggttctggccctga 239
QY 240 AGATTTGGCACTTATATATATATATATATATATATATATATATATATATATAT 299
Db 240 ga 241
QY 300 GA 301
RESULT      8

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LOCUS       R69532             463 bp     mRNA             EST             01-JUN-1995
DEFINITION  Y93178 r1 Homo sapiens cDNA clone 155249 5' similar to gb:U64338
            IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION   R69532
NID         Q843049
KEYWORDS    EST.
SOURCE      human clone-155249 library-Soares breast 2N-Rest vector-pET7710
            (Pharmacia) with a modified polylinker host-HIGH (ampicillin
            resistant) primer-M33P1 Psitel-Not I Psitel-Eco RI Adult female.
            1st strand cDNA was primed with a Not I - oligo(dT) primer (5'-
            TGTACCAATCTGAATGGAGGAGCGCGCCCTTTTCTTTT-3'),
            double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
            digested with Not I and cloned into the Not I and Eco RI sites of a
            modified pET771 vector (Pharmacia). Library went through one round
            of normalisation to a set = 230. Library constructed by Bento
            Soares and M.Fatima Beraldo.
ORGANISM    Homo sapiens
Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 463)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,P., Williamson,A., Wohlmann,P. and
            Wilson,P.
TITLE       The WashU-Merck EST Project
JOURNAL     Unpublished (1995)
COMMENT     Contact: Wilson PK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 394
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             source
                     1..463
                     /organism="Homo sapiens"
                     /clone="155249"
BASE COUNT   103 a 125 c 115 g 114 t      6 others
ORIGIN
Query Match      41.0%   Score 130; DR 24; Length 463;
Best Local Similarity 75.6%   Pred. No. 2 120-225;
Matches 189; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
Db 89 ctccagccacctgtgtgtgtctccagggaagagaccacctctctcagacacacac 148
QY 17 CTCATGTCCTCTGTGTGTAATGTCGAGACAGACACCAATATCTTCCTGGGGAATC 76
Db 149 agactgtgacttgaatttagctgtaccagcagaaacctgagcaggtctccagntcc 208
QY 77 AGACTATTAGCAGACACTTAATATGATATCAGTAAATCAGACACACACACACAC 136
Db 209 tctctatgtgtgcatctcctcagcagcagcagcagcagcagcagcagcagcagcag 268
QY 137 TGATATATGTGTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 196
Db 269 ctggagcagagcttctctcagcagcagcagcagcagcagcagcagcagcagcag 328
QY 197 CTGGGACAGATTTCTCATCATCATCATCATCATCATCATCATCATCATCATCAT 256
Db 329 attgtcagca 338
QY 257 ATTGTCAACA 266

```

	R69482	210 bp	mRNA	EST	01 JUN-1995
LOCUS	yj83c03.r1		Homo sapiens cDNA clone	155332.5	similar to gb:L09085
DEFINITION					

Q787047

ORGANISM

TITLE	JOURNAL	COMMENT
-------	---------	---------

[illegible]

Db 101

RESULT	1
LOCUS	
DEFINITION	
ACCESSION	
NID	
KEYWORDS	
SOURCE	

Q787047

ORGANISM

TITLE	JOURNAL	COMMENT
-------	---------	---------

FEATURES SOURCE

	BASE COUNT	ORIGIN
1	0.000	0.000
2	0.000	0.000
3	0.000	0.000
4	0.000	0.000
5	0.000	0.000
6	0.000	0.000
7	0.000	0.000
8	0.000	0.000
9	0.000	0.000
10	0.000	0.000
11	0.000	0.000
12	0.000	0.000
13	0.000	0.000
14	0.000	0.000
15	0.000	0.000
16	0.000	0.000
17	0.000	0.000
18	0.000	0.000
19	0.000	0.000
20	0.000	0.000
21	0.000	0.000
22	0.000	0.000
23	0.000	0.000
24	0.000	0.000
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95	0.000	0.000
96	0.000	0.000
97	0.000	0.000
98	0.000	0.000
99	0.000	0.000
100	0.000	0.000

Query: Max
Best: Local

Db 101

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DB 227

124 QY

DB	781
On	101

RESULTS
LOCUS
DEFINITION

ACCESSION

KEYWORDS
SOCIETY

of normalization to a Cot = 20. Library constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM

Homo sapiens
Euparietidae: Metazoa: Pomeroyia: Bilateria: Coelomata:
Centroscopia: Chordata: Vertebrata: Gnathostomata: Osteichthyes:
Sarcopterygii: Chonata: Tetrapoda: Amniota: Mammalia: Theria:
Eutheria: Archonta: Primates: Catarrhini: Hominoidea: Homo:
1 (bases 1 to 213)

REFERENCE
AUTHORS

Hillier, L., Clark, N., Duboucq, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, I., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
JOURNAL
COMMENT

The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway Box 8501 St. Louis, MO 63109
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 133

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

Location/Qualifiers
1..213
/organism="Homo sapiens"
/clone="161395"

BASE COUNT 51 a 55 c 49 g 55 t 2 others
ORIGIN

Query Match 34.4%; Score 109; DB 64; Length 213;
Best Local Similarity 81.9%; Pred. No. 6.46e-179;
Matches 145; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

Db 1 cccctgaactcctaactatggtggtccgaattacagagtggtcccaatcaagattca 60
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QY 125 cccctgaactcctaactatggtggtccgaattacagagtggtcccaatcaagattca 184
Db 61 gccgcagtgatgtggcagcagatttcactctccatccatccatccatccatccatccat 120
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QY 185 gtggcagtgatgtggcagcagatttcactctccatccatccatccatccatccatccat 243
Db 121 ttcccaacttattctcccaadgattacactctctctctctctctctctctctctctct 177
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QY 244 ttcccaacttattctcccaadgattacactctctctctctctctctctctctctctct 300

Search completed: Tue Feb 24 09:04:59 1998
Job time : 215 secs.

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26-SEP-1995 (first entry)
S43434 VK-I gene.
Graves ophthalmopathy associated immunoglobulin protein:
orbital antigen; monoclonal antibody; light chain; L chain;
variable region; autoimmunity; ss.
Homo sapiens.
W09508345-A.
30-MAR-1995.
22-SEP-1994; m10756
22-SEP-1994; SS-12446
(NICH-) NICHOLS INST DIAGNOSTICS
Melachian SM. Report B:
WJL 05-130283/18
P-PSPB: P72055.

Graves' ophthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR

Disclosure: Page 59; 94pp; English.

L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 14/15 clones of L chain (kappa) regions showed homology to the putative VK germline gene KJ012 (given in Q89317) and also to the S43434 VK-I gene used in a myasthenia gravis striational muscle autoantibody of thymic B-cell origin; the DNA (Q89318-23) and corresp amino acid (P72059-64)

sequences of 6 clones (QF7K.3, 15, 11, 9, 19 and 17) are provided.

Sequence 285 BP: 76 A; 78 C; 52 G; 59 T:

Query Match 77.3%; Score 247; DB 14; Length 285;
Best Local Similarity 94.2%; Pred. No. 1,52e+155;
Matches 262; Conservative 0; Mismatches 16; Indels 0; Gaps

8 agatgaccagcttcacactccctcgtcgatctgtgtagagacagatcaccatcaatt 57
5 AGGTACCCAGCTTCATGTCGCCCTGGTGAATTGGTAGACAGACTCACCATCACTII 64
68 ccccgcgaactccggcattaggcagtatttaaatctgatccagaacaacagggaaag 127
55 GCCTAGC-AAVLTCAAATAAAGAACTTAATCGSIATAGCA-AAAACAGGACAGA 124
128 cccttgaagctccctgaaccttatgtgataccaattttgcaaaatttgaggtccctaagtttta 197
125 CCCTTAAGGCCTCTSATTTATCTTGATCATCACTTTTC AAAAGTGGSGTTCCTACAGTTCA 194
188 gtgccagtggatctgggacagatttcactctccaccatccagcagtctgcacctcgaagatt 247
185 GTGCAGCTGATCTGGACAAGAAITTCATCTACCATATCACTGCTAACCTTGAAGAAAT 244

248 ttgcaacttactactgtcaacagatbtacagtaccccc 285
245 TTGCAGCTTACTTCTGTAAGAAAGAAITTCATCAAGCTTCAAAAGCTTCA 292

RESULT	5	
ID	T61240	standard. DNA: 705 BP.
AC	T61240:	
DE	13-MAY-1997	(first entry)
DT	Human anti-PSV monoclonal antibody RF-1	light chain DNA.
DI	Monoclonal antibody: MA5: PF-1: PF-2: respiratory syncytial virus;	
DD	RSV: fusion protein; F-protein; vaccine; immunotherapy; therapy;	
KK	Epstein Barr virus; immortalisation; recombinant antibody; SS.	
OS	Homo sapiens.	
Key	Location/Qualifiers	
RFH	sig_peptide	
FT	/*tag= a	1..60
FT	mat_peptide	61..702
FT	/*tag= b	
PN	W09640252-A1.	
PD	19-DEC-1996.	
PF	06-JUN-1996.	010076
PR	07-JUN-1995:	US-488376.
PA	(IDEC-) IDEC PHARM CORP.	
PI	Brams P, Chamat SS, Heard CJ, Newman RA, Pan L;	
PI	Walsh EE;	

WPI: 97-090902/09.
P-PSDB: W11638.
Human monoclonal antibody specific for respiratory syncytial virus fusion protein - used for the prevention and treatment of RSV infection
Claim 9, Fig 9a, 85pp, English.
A DNA sequence (161240) codes for a polypeptide (W11638) comprising a leader sequence, R1 light chain variable region (see also W11634), and human kappa constant region. PFI is a human monoclonal antibody (hMAK) specific for the fusion protein of respiratory syncytial virus (RSV). The DNA sequence, in vector NEOSPLA, can be used to produce the light chain construct in transfected embryonic (e.g. CHO) cells. PFI-1 and PFI-2 heavy and light chain constructs (see also 161241-42, 161279) are similarly used. The transfected host cells provide a constant stable supply of anti-RSV F-protein hMAbs for use in the treatment or prevention of RSV infection.
Sequence 705 BP: 178 A; 190 C; 177 G; 151 T;

Query Match 77.9%; Score 247; DB 28; Length 705;
Percent local similarity 89.2%; Posed No. 1 526-155;
Matches 280; Conservative 0; Mismatches 34; Indels 0; Gaps

68 agatgaccagcttcacatccctcgtctgcatctgtgagacagaggtcacctcactt 127
5 AGGTCACCCAGTTCATGTCCTCTGTCATTTGINSAGACAGAGTCACCATCAGT 64

128 gccggcgagctcgagagagatgtatttatttatttggatctccacccacacagaaag 187
65 GCGCGGCGAGCTCGAGAGATGTATTATTATTATGATGAGAACTTAAATTTGATCAAGAAAGAGAGACAG 124

188 cccctaaagctccctgatgatgtggtgacaaattggcacctggaggtccagtcgaagtcca 247
125 GCGCTAAAGCTCCCTGATGATGTGGTACAAATTTGCAAGATGGAGATGCCATCGAGAGTCA 184

248 gtggcggtgagctgggacagatttcactctcacacatgacagctctgcaacccagagat 307
185 GTGGCGGTGAGCTGGGACAGATTTCACTCTCACACATGACAGCTCTGCAACCTGCAACGATT 244

308 ttggaacttactattctcagagggttcagatgacccctcgaactttgggcccaggaacca 367
245 TTGGAATTACTATTCTCAGAGGTTCAAGATGAGATTAACAACCTTTGGGAACTTTGSCAAGAGACCA 304

368 aggtggaaatcaaa 381
305 AGGTGGAAATCAAA 318

RESULT 6
ID: Q89317 standard; DNA; 285 BP.
AC Q89317;
DE 26-SEP-1995 (first entry)
DE K1012 VK germline gene.
KW Graves ophthalmopathy associated immunoglobulin protein;
KW orbital antigen; monoclonal antibody; light chain; L chain.
KW variable region; autoimmunity; ss.
KW Homo sapiens.
KW WO9508336-A.
PN PPN
PD 30-MAR-1995.
PF 22-SEP-1994; U10756
PF 22-SEP-1993; US-124469
PR 22-SEP-1993; US-124469
PR (NICH-) NICHOLS INST DIAGNOSTICS.
PI McLaughlin SM, Rapoport B;
PI wpi: 95-139383/18.
PI P-PSDB: R72058.
PI Graves' ophthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR
PI Disclosure, page 56, 94pp, English.
PS L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 14/15 clones of L chain (kappa) regions showed homology to the putative VK germline gene K1012.
SC Sequence 285 BP: 75 A; 63 G; 70 T;
SC wpi: 95-139383/18.

Query Match 77.6%, Score 246, DB 14, Length 285,
 Best Local Similarity 94.9%, Pred. No. 8, 02e-155;
 Matches 259, Conservative 0, Mismatches 14, Indels 0, Gaps 0.

Db 13 accaggtccatccctccctgctgcatctgttagagacagagatccatccatccctgcccgg 72
 QY 10 ACCCAGTCCATCGTCCCTGCTGTCATTTGTNGGACAGAGATCCACATCACTTCCCGG 69
 Db 73 gcaactcagacattagcagctatttaattggtatcagcagaaacccaggaaagccct 132
 QY 70 GCAAGTCAGAGATTAGCAGAACTTAATTTGTTATCAGCAGAAATCAGAGCCCT 129
 Db 133 aagctccctgcatctgctgcatccagttgcaagtggtgggtcccatcacaaggttcadtgcc 192
 QY 130 AAGGTCCTCATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCGAGGTTCACTGGC 189
 Db 193 agtgatctggagacagatttccactctcaccatcagcagctgcaacctgaagattttgca 252
 QY 190 AGTGATCTGGCAGAGATTTTCACTCTTACCATCCAGTCTGCAAGCTGCAAGATTTTGA 249
 Db 253 acttactactgcaacagagttacagttacccct 285
 QY 250 ACTTACTATTCTCACAGAGTTACACAGCCCT 292

RESULT 7
 ID T61236 standard; DNA; 321 BP.
 AC T61236;
 DT 13-MAY-1997 (first entry)
 DE Human anti-RSV monoclonal antibody RF-1 VL domain DNA.
 KW Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus;
 KW RSV; fusion protein; F-protein; vaccine; immunotherapy; therapy;
 KW Epstein Barr virus; immortalisation, recombinant antibody; ss.
 OS Homo sapiens.
 PN W09640252-A1.
 PD 19-DEC-1996.
 PF 06-JUN-1996; U10070.
 PR 07-JUN-1995; US-488376.
 PA (IDEC-) IDEC PHARM CORP.
 PI Brans P, Chamat SS, Heard CJ, Newman PA, Pan I;
 PI Walsh EE;
 DP WPI: 97-09892/09.
 DR P-PSDR: W11634.
 PT Human monoclonal antibody specific for respiratory syncytial virus
 PT fusion protein - used for the prevention and treatment of RSV
 PT infection
 PS Claim 9: Fig 7a; 85pp; English.
 CC Nucleic acids (T61236-39) respectively code for the RF-1 VL domain,
 CC RF-2 VH domain, RF-2 VL domain and RF-1 VH domain (W11634-37) of
 CC human monoclonal antibodies (hMAbs) RF-1 and RF-2, which show high
 CC affinity for respiratory syncytial virus (RSV) fusion protein. The
 CC hMAbs were obtd. by: antigen priming of naive human splenocytes in
 CC vitro; transferal of the primed splenocytes to a SCID mouse;
 CC boosting with antigen; isolating human antibody-producing B-cells
 CC from the SCID mice; and immortalisation of the B-cells using
 CC Epstein Barr virus. DNA encoding the RF-1 and RF-2 heavy and
 CC light variable domains can be incorporated into vectors (e.g.
 CC NEOSPIA) and used to transfect eukaryotic (e.g. CHO) cells (see
 CC also T61240-42, T61279) to provide a constant, stable supply of
 CC anti-RSV F-protein hMAbs for use in the treatment or prevention of
 CC RSV infection.
 SQ Sequence 321 BP: 82 A: 50 C: 72 G: 77 T: 1;

Query Match 76.0%, Score 241, DB 28, Length 321;
 Best Local Similarity 88.2%, Pred. No. 3, 32e-151;
 Matches 277, Conservative 5, Mismatches 37, Indels 0, Gaps 0.

Db 8 agatgaccagctccatccctccctgctgcatctgttagagacagagatccatccatccct 67
 QY 5 AGCT-ACCGAGTCTCCATCGTCCCTGCTGTCATTTGNGGACAGAGATCCACATCACT 64
 Db 68 cccggagggtcagaggattctagttatttaattggtatcagcagaaacccaggaaag 127

QY 65 GGGGGGAACTAGATATTAAGCAGGAACTTAATTTGGTATCAGCAGAAATCAGTCAAG 124
 Db 128 cccctaagctccctgatatgtggtggtggtggtggtggtggtggtggtggtggtggtggt 187
 QY 125 CCGCTAAGGTCCTGATCTATGCTGATCCAGTTTGCAGAGTGGGCTGATATTAAGGTTCA 184
 Db 188 gtggcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 247
 QY 185 GTGGCAGTGTGATCTGGCAGATTTTCACTTCTACCATCACTAGTGTGATCTCAAGATT 244
 Db 248 ttgcaacttct 307
 QY 245 TTGCAACTTCTACTTATTCACACAGAGTTACACAAACCCCTGGAGGTTGGGTCAGGATCA 304
 Db 308 aggtgggaatcaaa 321
 QY 305 AGGTGGAGTCAAA 318

RESULT 8
 ID T60371 standard; DNA; 324 BP.
 AC T60371;
 DT 27-NOV-1997 (first entry)
 DE Anti-TGF beta-2 scfv antibody 6-H1 VL gene.
 KW Transforming growth factor beta-2; TGF-beta-2; human;
 KW antibody engineering; scfv; phage display; lung fibrosis;
 KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular diseases; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection, therapy, chain shuffling, ss.
 OS Chimeric Homo sapiens;
 OS Chimeric synthetic.
 PN GB2305921-A.
 PD 23-APR-1997.
 PF 07-OCT-1996; 020920.
 PR 19-JAN-1996; GB-001081.
 PA 06-OCT-1995; GR-020486.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L, Green JA, Jackson PH, Johnson KS, Pope AP;
 PI Tempest PP, Thompson JE, Vaughan TJ, Williams AJ;
 PI Wilton AJ;
 DP WPI: 97-215360/20.
 DR P-PSDB: W15524.
 PT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
 PT immune and inflammatory disease
 PS Example 1: Fig 2b(i); 184pp; English.
 CC This DNA sequence comprises the gene encoding the VL domain
 CC (W15524) of human scfv antibody 2A-H1 (also known as 6H1), which
 CC is specific for transforming growth factor (TGF) beta-2. It was
 CC isolated from a light chain shuffle repertoire of a peripheral
 CC blood lymphocyte library. The antigen-binding domains of human
 CC antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can be used
 CC to counter the adverse effects of TGF beta, such as (i) promotion
 CC of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis,
 CC arterial injury, proliferative retinopathy, retinal detachment,
 CC adult respiratory distress syndrome, liver cirrhosis, post
 CC myocardial infarction, post-angioplasty restenosis, scleroderma,
 CC vascular disorders, cataract, glaucoma, or esp. neural scarring and
 CC glomerulonephritis, also (not claimed) osteoporosis), or (ii)
 CC immune and inflammatory diseases (e.g. rheumatoid arthritis,
 CC macrophage deficiency diseases or macrophage pathogen infection).
 CC Nucleic acids encoding human antibody VH and VL can be used for
 CC prodn. of recombinant antigen-binding domains. These are highly
 CC specific, have low dissociation constants (pref. less than 5 nM)
 CC and low IC50s for neutralisation.
 SQ Sequence 324 BP: 90 A: 82 C: 74 G: 78 T: 1;

QY 16 AACCAGTCTCATGATGTCCTGTCGCAATTTGTTGAGACAGCAATCAATCATCACTTTGCGGG 64
 Db 73 gcaactcagaggtattagtaactggttgccctgtgtatcacagaaaccacagagagccct 132
 QY 70 GCAAGTCAGAGTATTACAGAGCACTTAATTTGTTATCACAGAAACCAGGACAGCCCT 129
 Db 133 aagctcttgatctataaaggcatctactttagaaaggggtcccatcaaggttttagggc 192
 QY 130 AAGTCTCTGATCTATGCTGCATCCAGTTTGCAGAACTGGGTCCCATCGAGGTTCAAGTGGC 189
 Db 193 agtgatctcagcagagatttcaactctcaccatcagcagctgtcgaacctgaagattttaca 252
 QY 190 AGTGGATCTGGGACAGATTTCACTCTCAGCATCACAGCTCTGCAACTCGAAGATTTTGCA 249
 Db 253 acttaactactgtaacagagttacagaccctggaacttcggccaaaggaccagagct 312
 QY 250 ACTTACTATTGTCANACAGAGTTACACAAACCCCTCGAGCTGGCCAGGACCAAGGTG 309
 Db 313 gagatcaaa 321
 QY 310 GAAGTCAAA 318

RESULT 11
 ID T60123 standard: cDNA: 341 BP.
 AC T60123;
 DE 15-MAY-1997 (first entry)
 DE Coding sequence for light chain #4.
 KW Antibody; heavy chain, light chain, variable region; human, monoclonal.
 KW Complementarity determining region, human, adr type hepatitis B virus.
 KW HB virus; CDR, virus antigen, anti-HB antibody; vaccine; ss.
 OS Homo sapiens.
 PN J09020798-A.
 PD 21-JAN-1997.
 PF 11-JUL-1995; 174752.
 PR 11-JUL-1995; JP-174752.
 PA (ASAH) ASAH KASEI KOGYO KK.
 DR WPI: 97-140911/13.
 DR P-PSDB; W13028.
 PT Human anti-Hepatitis B antibody - used in a adr type HB virus vaccine
 PS Claim 10; Page 17; 20pp, Japanese.
 CC T60116-T60123 represent the coding sequences for the heavy and light chains of the human monoclonal antibody of the invention. The antibody of the invention preferably contains the sequence represented by W13912 in the complementarity determining region-1 (CDR-1) of the heavy chain variable region. The antibody of the invention also contains the sequence represented by W13913 in the CDR-3 of the light chain variable region. The antibody is capable of binding to adr type hepatitis B (HB) virus antigen. A human anti-HB virus monoclonal antibody preparation which is highly safe and is effective to adr type HB virus can be provided, using the monoclonal antibody. It can also be used as a vaccine against HB infection. It can also be used as a

Query Match 75.1%; Score 238; DP 28; Length 341;
 Best Local Similarity 87.6%; Pred. No. 4, 90e-149;
 Matches 276; Conservative 0; Mismatches 33; Indels 0; Gaps 0.
 Db 4 gagtgaccagct 63
 QY 4 GAGTCAACCAAGTCTCATGTCCTGTCGCAATTTGTTGAGACAGCAATCAATCATCACTTT 63
 Db 64 tgccgggcaagtcagacagcttgaacacatttgaattggtatcgccaaagccaggaaa 123
 QY 64 TGCCGGGCAAGTCAGAGTATTAGTAGAGCAATTTAAATTTGTTATTCATCAATCAATCA 123
 Db 124 gccctcaacctcctgatctatgtctgcatccagtttgcaagtggggtcccatcaaggttc 183
 QY 124 GCCCTCAAGCTCCTGATCTATGCTGCATCCAGTTTGCAGAACTGGGTCCCATCGAGGTT 183
 Db 184 attgacagtgatctgagacagatttcaactctcaccatcaactctctcgaacctgaagat 243
 QY 184 attgacagtgatctgagacagatttcaactctcaccatcaactctctcgaacctgaagat 243

QY 184 AGTGGAGTGGATCTGGAGACAGATTTCACTCTCAGCATCACAGCTCTGCAACTCGAAG 243
 Db 244 ctgcaactctatctgtcaacagctgttagcatccctctgacacattcggccagggagcc 303
 QY 244 TTGGAACTTATATGTCAGACAGATTTAAACAGCCCTCGGAGTGGGAGTAAAGGAGC 303
 Db 304 aggtggagacataaa 318
 QY 304 AAGGTGGAAGTCAAA 318
 RESULT 12
 ID T60121 standard: cDNA: 338 BP.
 AC T60121;
 DE 15-MAY-1997 (first entry)
 DE Coding sequence for light chain #3.
 KW Antibody; heavy chain, light chain; variable region; human; monoclonal.
 KW Complementarity determining region; human; adr type hepatitis B virus;
 KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine; ss.
 OS Homo sapiens.
 PN J09020798-A.
 PD 21-JAN-1997.
 PF 11-JUL-1995; 174752.
 PR 11-JUL-1995; JP-174752.
 PA (ASAH) ASAH KASEI KOGYO KK.
 DR WPI: 97-140911/13.
 DR P-PSDB; W13926.
 PT Human anti-Hepatitis B antibody - used in a adr type HB virus vaccine
 PS Claim 9; Page 14; 20pp, Japanese.
 CC T60116-T60123 represent the coding sequences for the heavy and light chains of the human monoclonal antibody of the invention. The antibody of the invention preferably contains the sequence represented by W13912 in the complementarity determining region-1 (CDR-1) of the heavy chain variable region. The antibody of the invention also contains the sequence represented by W13913 in the CDR-3 of the light chain variable region. The antibody is capable of binding to adr type hepatitis B (HB) virus antigen. A human anti-HB virus monoclonal antibody preparation which is highly safe and is effective to adr type HB virus can be provided, using the monoclonal antibody. It can also be used as a vaccine against HB infection. It can also be used as a

Query Match 74.1%; Score 235; DP 28; Length 338;
 Best Local Similarity 89.5%; Pred. No. 7, 23e-147;
 Matches 282; Conservative 0; Mismatches 30; Indels 3; Gaps 2.
 Db 4 gagtgaccagct 63
 QY 4 GAGTCAACCAAGTCTCATGTCCTGTCGCAATTTGTTGAGACAGCAATCAATCATCACTTT 63
 Db 64 tgccgggcaagtcagacagcttgaacacatttgaattggtatcgccaaagccaggaaa 123
 QY 64 TGCCGGGCAAGTCAGAGTATTAGTAGAGCAATTTAAATTTGTTATTCATCAATCAATCA 123
 Db 124 gccctcaacctcctgatctatgtctgcatccagtttgcaagtggggtcccatcaaggttc 183
 QY 124 GCCCTCAAGCTCCTGATCTATGCTGCATCCAGTTTGCAGAACTGGGTCCCATCGAGGTT 183
 Db 184 aggtggagctgtgtgtacagatttcaactctcaccatcagcagctctcgaacctgaagat 243
 QY 184 AGTGGAGTGGATCTGGAGACAGATTTCACTCTCAGCATCACAGCTCTGCAACTCGAAG 243
 Db 244 ttgcaacttaactgtcagacagatttcaactctcaccatcagcagctctcgaacctgaag 300
 QY 244 TTGCAACTTAACTATGTCAGACAGATTTAAACAGCCCTCGGAGTGGGAGTAAAGGAGC 303
 Db 301 aggtggagctcaaa 315
 QY 304 AAGGTGGAAGTCAAA 318
 RESULT 13

CC for production of an anti-hepatitis B virus surface antigen antibody by
CC ELISA. The MAb's are then purified from large scale cell culture by
CC protein A chromatography, size separation on Sephacryl S300 gel and ion
CC exchange chromatography on Q-Sepharose. The heavy and light chains of
CC the MAb's were isolated and their amino acid sequences determined.
CC Primers were generated and used to amplify cDNA synthesised from RNA
CC purified from each hybridoma cell line. The sequences of the heavy and
CC light chains (nucleic acid and amino acid) from MAb's PEI-1, 2M1-1, 2M1-2
CC and MD3-4 are shown in T8538-45 and W24984-91. The MAb's can be used to
CC treat HBV infections in immunosuppressed patients or patients with
CC chronic active hepatitis, especially liver transplant patients.
SQ Sequence 384 BP; 83 A; 108 C; 100 G; 93 T;

Query Match 72.2%; Score 229; DB 33; Length 384;

Best Local Similarity 86.3%; Pred. No. 1.56e-142;

Matches 271; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Db 68 agatgaccagctccatctccgtgtctgcattgtgtgggagacagagtcaccgtcactt 127

QY 5 AGCTACCCAGTCTGCATCGTCCCTGCTGTGTGATTTGTNGGACACAGAGTCACCATCACTT 64

Db 128 gtggggcaggtcaggtattagcagttggttagcctgtatcagcagaaaccagggaag 187

QY 65 GCCGGCAAGTCAGAGTATTAGCAGGAACCTAAATTGTTATCAGCAGAAACCAGGGACAG 124

Db 188 cccctaaactctgcattcgcattcccaatttgcacaaagtgggtcccatcaagggttca 247

QY 125 CCCCCTAAGGTCTGTGATCTATGTGCTCATCCAGTTTGCAAAGTGGGTCCTCCATCGAGGTTCA 184

Db 248 tcggcagtgatctgggacagatttcactctcaccatcaccagcctgcaggctgaagatt 307

QY 185 GTGGCAGTGGATCTGGGACAGATTTCACCTTCACCATCACCAGTCTGCAACCTGAAGATT 244

Db 308 ttgcaacctactattgtcaacagggtgacagctctcccttttacttttcggcgaggagacca 367

QY 245 TTGCAACTTACTATTGTCAACAGAGTTACACAACCCCTCGGACCTTCGGCCAAAGGGACCA 304

Db 368 aggtgacttcaaa 381

QY 305 AGGTGGAAGTCANA 318

Search completed: Tue Feb 24 09:01:01 1998

Job time : 62 secs.

WATERMAN

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit
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MPSrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 08:49:27 1998: Waspar time 136.04 seconds
Tabular output not generated. 689.884 Million cell updates/sec

Title: >US-08-844-215-19
Description: (1-372) from US08944215.seq
Perfect Score: 372
N.A. Sequence: 372
Comp: 1 GAGCTGCACGCTTCGAGATC
GAGCTGCACGCTTCGAGATC

Scoring table: TABLE default
Gap 6

Nmatch STD - Dbase 0: Query 0
Searched: 333433 seqs, 125143548 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: STS
1:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8
9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19
20:STS20 21:STS21 22:STS22 23:STS23 24:STS24
25:STS25 26:STS26 27:STS27 28:STS28 29:STS29
30:STS30 31:STS31 32:STS32 33:STS33 34:STS34
35:STS35 36:STS36 37:STS37 38:STS38 39:STS39
40:STS40 41:STS41 42:STS42 43:STS43 44:STS44
45:STS45 46:STS46 47:STS47 48:STS48 49:STS49
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70:STS70 71:STS71 72:STS72 73:STS73 74:STS74
75:STS75 76:STS76 77:STS77 78:STS78 79:STS79
80:STS80 81:STS81 82:STS82 83:STS83 84:STS84
85:STS85 86:STS86 87:STS87 88:STS88 89:STS89
90:STS90 91:STS91 92:STS92 93:STS93 94:STS94
95:STS95

Statistics: Mean 9.950 Variance 1.948 Scale 5.112

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Length	DB ID	Description	Pred. No.
1	84	22.6	597 24	AA472093	510305 r1 Soares mouse
2	84	22.6	597 23	AA472093	510305 r1 Soares mouse

C	3	76	20.4	435 80	HSAA7475	dh76c05.s1 NCI_CGAP_H	1.18e-98
C	4	76	20.4	435 40	AA507475	dh76c05.s1 NCI_CGAP_H	1.18e-98
C	5	54	14.5	269 54	HS120138	z447b07.r1 Soares ova	3.39e-57
C	6	54	14.5	269 54	HS120138	z447b07.r1 Soares ova	3.39e-57
C	7	33	8.9	238 69	HS1300461	aa63q01.r1 NCI_CGAP_G	3.46e-21
C	8	33	8.9	238 35	AA505044	aa63q01.r1 NCI_CGAP_G	3.46e-21
C	9	29	7.8	211 63	HS1209634	zx83b07.r1 Soares ova	4.40e-15
C	10	29	7.8	211 17	AA504794	zx83b07.r1 Soares ova	4.40e-15
C	11	23	6.2	259 56	HS1201117	ab12f07.r1 Stratagene	9.95e-07
C	12	23	6.2	259 30	AA488343	ab12f07.r1 Stratagene	9.95e-07
C	13	22	5.9	156 1	DM36D7S	D. melanogaster STS d	1.86e-05
C	14	21	5.6	189 18	AA455361	aa23c11.s1 NCI_CGAP_G	3.13e-04
C	15	21	5.6	189 63	HS1205169	aa23c11.s1 NCI_CGAP_G	3.13e-04
C	16	21	5.6	304 22	AA293024	z118b00.s1 NCI_CGAP_G	3.13e-04
C	17	21	5.6	304 57	HS1187557	z118b00.s1 NCI_CGAP_G	3.13e-04
C	18	21	5.6	400 78	HSAA51414	z118b00.s1 NCI_CGAP_G	3.13e-04
C	19	21	5.6	551 56	HS1214338	z118b00.s1 NCI_CGAP_G	3.13e-04
C	20	20	5.4	372 39	AA501612	ng17g10.s1 NCI_CGAP_L	4.75e-03
C	21	20	5.4	372 69	HS1207523	ng17g10.s1 NCI_CGAP_L	4.75e-03
C	22	20	5.4	354 66	HS1207593	nf07a07.s1 NCI_CGAP_L	4.75e-03
C	23	20	5.4	354 32	AA484418	nf07a07.s1 NCI_CGAP_L	4.75e-03
C	24	20	5.4	475 10	HS1244837	z27a05.r1 Soares ova	4.75e-03
C	25	20	5.4	540 25	AA475527	z27a05.r1 Soares ova	4.75e-03
C	26	20	5.4	540 94	MM1266847	z27a05.r1 Soares ova	4.75e-03
C	27	20	5.4	563 57	HS1228508	z27a05.r1 Soares ova	4.75e-03
C	28	20	5.4	597 51	AA280060	z27a05.r1 Soares ova	4.75e-03
C	29	20	5.4	597 51	HS118459	z27a05.r1 Soares ova	4.75e-03
C	30	20	5.4	630 80	HSAA8544	z27a05.r1 Soares ova	4.75e-03
C	31	20	5.4	736 45	AA480703	SMFCA2052SK Brugia m	4.75e-03
C	32	20	5.4	736 45	BM1273026	SMFCA2052SK Brugia m	4.75e-03
C	33	19	5.1	73 50	HS1166501	zsl1e10.s1 NCI_CGAP_G	6.39e-02
C	34	19	5.1	73 50	AA251793	zsl1e10.s1 NCI_CGAP_G	6.39e-02
C	35	19	5.1	169 12	HUMSWS574	human chromosome 7 ST	6.39e-02
C	36	19	5.1	223 61	HS1251854	human STS WI-304	6.39e-02
C	37	19	5.1	336 2	G03771	human STS WI-304	6.39e-02
C	38	19	5.1	343 54	HS1206924	zvl1g05.s1 Soares Nhh	6.39e-02
C	39	19	5.1	363 65	HS1273041	zvl1g05.s1 Soares Nhh	6.39e-02
C	40	19	5.1	410 81	MM1250713	vf80h12.r1 Soares mou	6.39e-02
C	41	19	5.1	423 70	HS1300938	vf80h12.r1 Soares mou	6.39e-02
C	42	19	5.1	442 76	HSAA36248	zr83g12.s1 NCI_CGAP_H	6.39e-02
C	43	19	5.1	524 9	G20434	zr83g12.s1 NCI_CGAP_H	6.39e-02
C	44	19	5.1	576 34	AA501010	human STS SHG3-33500	6.39e-02
C	45	19	5.1	836 42	AA522502	z118b00.s1 NCI_CGAP_L	6.39e-02

ALIGNMENTS

RESULT	1	AA472093	597 bp	mpna	EST	18-JUN-1997
LOCUS		vh10a05.r1	Soares mouse mammary gland	NDMMG	Mus musculus cDNA clone	
DEFINITION		975724 bp, similar to rat 5676115 GAMMA 2 CHAIN cation (gamma2)				
		975724 bp, similar to rat 5676115 GAMMA 2 CHAIN cation (gamma2)				
		region (MOUSE):				
ACCESSION		AA472093				
KEYWORDS		EST				
SOURCE		house mouse				
ORGANISM		Mus musculus				
REFERENCE		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS		1 (bases 1 to 597)				
		Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubayle, J., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, J., Lennon, G., Soares, B., Wilson, R. and Waterston, R.				
TITLE		The WashU-HM Mouse EST Project				
JOURNAL		Unpublished (1996)				
COMMENT		Contact: Marra M/Mouse EST Project				
		WashU-HM Mouse EST Project				
		Washington University School of Medicine				

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. RNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the IMA G.E. Consortium/LLNI at: www.bio.lnlnl.gov/btbp/image/image.html	
TITLE JOURNAL COMMENT	Insert Length: 558 Std Error: 0.00 Seq primer: -40ml3 fwd, ET from Amersham High quality sequence stop: 131.
FEATURES	Location/Qualifiers 1..435 /organism="Homo sapiens" /note="Vector: p7f13D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7f13 vector. Library is not normalized. (The "normalized version of this library is NCI_CGAP_Br2") Library was constructed by Bento Soares and M. Fatima Bonaldo."
SOURCE	/clone="964424" /sex="female, pooled" /tissue.type="breast" /lab_host="DH10B" cl...>435
BASE COUNT	94 a 128 c 112 g 101 t
ORIGIN	mRNA
Query Match	20.4% Score 76: DP 40: Length 435:
Best Local Similarity	83.5% Pred No 118e-98:
Matches	132 Conservative 0 Mismatches 20 Indels 6 Gaps 3
Dl	198 ataccctgagacccatcctagacaccttcctctggaggcgaggaaccccaactcatgccatcc 257
Cp	152 ATACCTGCCAGCACCCTCCAGGGCTTCGTGGATCTTGAGACTTGGGAGAACCATGCAATCAA 94
Dd	258 ccgatctgcataaatgataccccagagtctacaagagaattctcagaagaaatccagagc 317
Cp	62 --GC-ACTG---AAGSTTAATGAAATGTTTCACAGAGAGATGTCAGGAGATGCCAGAG 39
Dd	318 tgatcaccaagctcccacagatctccaacagtttgccacctc 355
Cp	38 TGGACCAAGCCCTCCGACAGCTGGAGACAGCTGCACCTC 1
RESULT	5
ID	HS1202138 standard; RNA: EST: 266 BP.
AC	AA402547;
NI	q2056386
DT	01-MAY-1997 (Pel 51, Created)
DT	22-MAY-1997 (Pel 52, Last updated, Version 2)
DE	z047h07.r1 Soares ovary tumor NBOT Homo sapiens cDNA clone 741181
DE	5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
KW	EST.
OS	Homo sapiens (human)
OC	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC	Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN	[1]
RP	1-266
RA	Hillier L., Allen M., Bowles L., Dubouque J., Geisel G., Post S., Kucaba T., Lacy M., Le N., Lennon G., Marrero M., Martin J., Parker A., et al.

```

RA Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
RA White Y., Willie T., Waterston R., Wilson R.;
RT "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel. 314 286 1800 Fax. 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28ml3 rev2 ET from Amersham.
FH Key
FH Location/Qualifiers
FT source
FT 1..266
FT /organism="Homo sapiens"
FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a
FT modified polylinker, Site_1, Not I, Site_2, Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer [5',
FT TGTTACCAATCTGAAGTGGGAGCGCGGTTTTTTTTTTTTTTT 3']
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT73 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M.Fatima Bonaldo."
FT /clone_lib="Soares ovary tumor NBHOT"
FT /sex="Female"
FT /tissue_type="ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
FT mRNA
FT <1..>266
FT Sequence 266 BP; 54 A; 90 C; 70 G; 52 T; 0 other;

Query Match 14.5%; Score 54; DB 54; Length 266;
Best Local Similarity 66.5%; Pred. No. 3,39e-57;
Matches 119; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

Db 38 agggcagatcaccctgacccaggggagcgtccacagacacactctacatgggctgagca 97
QY 194 AGGGCGGATTCACCTCTCCAGAGACAATTCACAGAACACCGCTTCTCTGCAATGAACA 253
Db 98 gctcagatctgagacacgcccgtgtattactatcgagagacgtttaccagctcgtcaa 157
QY 254 GCTTGAGCCGAGAGACAGCGGTGTCTATTATGTGAGACAGAGGTACTTTTGAGATGCA 313
Db 158 tccgcctcagctggtacttcgactctctggtggccgtgga-ccttggtcactgtctcctca 215
QY 314 TTAAGGGGCGTTACTACTTGAACACTGGGCGGAGAACCGCTGCTCACCCTCTCTCTCA 372

RESULT 6
ID HSI27079 standard; RNA; EST; 230 BP.
AC AA428970;
NI 92110596;
DT 25-MAY-1997 (Rel 52, Created)
DT 25-MAY-1997 (Rel 52, Last updated, Version 1)
DE cv49b02.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone 756939
DE 5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria, Primates, Catarrhini, Hominoidea;
RN [1]
RP 1-230
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
RA White Y., Willie T., Waterston R., Wilson R.;
RT "WashU-Merck EST Project 1997";
RL Unpublished
CC Contact: Wilson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel. 314 286 1800 Fax. 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28ml3 rev2 ET from Amersham.
FH Key
FH Location/Qualifiers
FT source
FT 1..230
FT /organism="Homo sapiens"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker, Site_1, Not I, Site_2, Eco RI; 1st strand cDNA
FT was prepared from human tonsillar cells enriched for
FT germinal center B cells by flow sorting (CD20+, IgD-),
FT provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
FT (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
FT primed with a Not I - oligo(dT) primer

```


[illegible]

DT 19-JUN-1997 (Rel. 52, Last updated, Version 1)
 DE aa23c11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 814100 3' similar
 DE to gb:D90209 DNA-BINDING PROTEIN TAXREB67 (HUMAN);.
 KW EST.
 OS Homo sapiens (human)
 OC Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
 OC Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP 1-189
 RA NCI-CGAP;
 RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 RT Tumor Gene Index";
 RL Unpublished.
 CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
 CC Robert_Strausberg@nih.gov This clone is available royalty-free
 CC through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
 CC for further information. Seq primer: -41ml3 fwd. ET from Amersham.
 CC Key
 FH Location/Qualifiers
 FT source
 FT 1..189
 FT /organism="Homo sapiens"
 FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 FT polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 FT was prepared from human tonsillar cells enriched for
 FT germinal center B cells by flow sorting (Cd20+, IgD-),
 FT provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 FT (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 FT primed with a Not I - oligo(dT) primer
 FT [5'-TGTTACCAATCTGAAGTGGGCGCGCTCATTTTTTTTTTTTTTTT-
 FT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (
 FT Pharmacia), digested with Not I and cloned into the Not I
 FT and Eco RI sites of the modified pT7T3 vector. Library was
 FT through one round of normalization, and was constructed by
 FT Bento Soares and M. Fatima Bonaldo."
 FT /clone="814100"
 FT /clone_lib="NCI_CGAP_GCB1"
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 FT /lab_host="DH10B"
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 FT mRNA
 SQ Sequence 189 BP; 32 A; 68 C; 59 G; 30 T; 0 other;
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 Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Db 119 gcacgcgagcgtctcgggacaccccaagcaagaccgcgtccc 163
 |||| ||| |||| |||| || || || |||| ||||
 Cp 68 GCACGAGGAGTCTCAGGAGACCTCCCGAGGCTGGACCGCCTCCC 24

Search completed: Tue Feb 24 08:51:58 1998
 Job time : 151 secs.

WATERMAN

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPstch_on n.a. - n.a. database search, using Smith-Waterman algorithm
Run On: Tue Feb 24 08:52:23 1998. MasPar time 426.60 Seconds
Tabular output not generated.

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N.A. Sequence: 1 GCGCTGAGTGGGTGAGAGG GCGCTGAGTGGGTGAGAGG
Comp: GCGCTGAGTGGGTGAGAGG GCGCTGAGTGGGTGAGAGG

Scoring table: TABLE default
Gap: Gap
Nmatch: 500 - Base 0: Every 0
Searched: 430261 seqs, 71021276 bases x 2
Post-processing: Minimum Match 0%
Listing first 4 summaries

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1: BCT1 2: FUN 3: GEN 4: HTG1 5: HTG2 6: HTG3 7: HTG4 8: HUM1
9: HUM2 10: HUM3 11: INV1 12: INV2 13: OPS 14: XAM 15: VPT
16: PUN1 17: PUN2 18: PUN3 19: PUN4 20: SYN 21: UNC 22: VPT
genbank101

Database: genbank101
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30: BCT8 31: BCT9 32: BCT10 33: BCT11 34: BCT12 35: BCT13
36: BCT14 37: BCT15 38: BCT16 39: BCT17 40: BCT18 41: BCT19
42: BCT20 43: BCT21 44: BCT22 45: BCT23 46: BCT24 47: BCT25 48: BCT26
49: BCT27 50: BCT28 51: BCT29 52: BCT30 53: BCT31 54: BCT32 55: BCT33
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142: BCT121 143: BCT122

Statistics: Mean 9.999 Variance 4.326 scale 2 291
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

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1	281	88.6	370	91	H.sapiens mRNA for Ig	5.546-214
2	280	88.3	348	91	H.sapiens rearranged	4.516-213
3	279	88.0	322	91	H.sapiens mRNA for Ig	4.126-212
4	277	87.4	429	99	Human Ig rearranged 1	3.536-210
5	274	86.4	326	99	Human Ig rearranged 2	2.596-217
6	273	86.1	346	91	H.sapiens rearranged 3	2.456-226
7	273	86.1	382	91	H.sapiens mRNA for Ig	2.456-226
8	272	85.8	325	99	Human Ig (thyroid) for	2.246-225
9	270	85.2	311	96	H.sapiens rearranged	1.866-213
10	269	84.9	322	91	H.sapiens mRNA for Ig	1.706-222
11	268	84.5	321	91	H.sapiens mRNA for Ig	1.556-221
12	269	84.5	322	99	Human Ig rearranged 3	1.556-221
13	268	84.5	326	99	Human Ig rearranged 3	1.556-221
14	268	84.5	348	91	H.sapiens rearranged	1.556-221
15	267	84.2	333	69	DNA encoding V _H region	1.416-220
16	267	84.2	345	93	H.sapiens mRNA for ka	1.416-220
17	265	83.6	321	101	Human IgM rearranged	1.176-218
18	264	83.3	321	96	H.sapiens B1P-Kg1.5a	1.076-217
19	264	83.3	311	96	H.sapiens rearranged	1.076-217
20	264	83.3	319	96	H.sapiens rearranged	1.076-217
21	263	83.0	326	91	H.sapiens immunoglobulin	1.076-217
22	262	82.6	321	96	H.sapiens rearranged	8.896-216
23	262	82.6	321	99	Homo sapiens (clone 3)	8.896-216
24	262	82.6	321	91	H.sapiens mRNA for Ig	8.896-216
25	262	82.6	325	99	Human Igk (thyroid) for	8.896-216
26	261	82.3	324	91	H.sapiens gene for Im	8.896-216
27	261	82.3	324	99	H.sapiens rearranged	8.896-216
28	260	82.0	311	96	H.sapiens rearranged	7.336-214
29	260	82.0	311	99	Human Igk (thyroid) for	7.336-214
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31	259	81.7	322	99	Human immunoglobulin	6.646-213
32	259	81.7	406	99	Human rearranged Igk	6.646-213
33	258	81.4	313	96	H.sapiens B2P3-Kg1-A	6.036-212
34	258	81.4	315	92	H.sapiens mRNA for va	6.036-212
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36	258	81.4	321	93	H.sapiens immunoglobulin	6.036-212
37	258	81.4	324	91	H.sapiens mRNA for va	6.036-212
38	258	81.4	327	93	H.sapiens mRNA for va	6.036-212
39	258	81.4	327	91	H.sapiens immunoglobulin	6.036-212
40	257	81.1	368	91	H.sapiens mRNA for va	5.496-211
41	257	81.1	368	95	Human immunoglobulin	5.496-211
42	256	80.8	315	102	Human immunoglobulin	4.486-210
43	256	80.8	315	91	H.sapiens mRNA for va	4.486-210
44	256	80.8	315	91	H.sapiens immunoglobulin	4.486-210
45	255	80.4	370	91	H.sapiens mRNA for va	4.486-210

ALIGNMENTS

RESULT 1 HSLKLV20 370 bp PNA PPT
Locus H.sapiens mRNA for rearranged Ig kappa light chain variable region
DEFINITION H.sapiens mRNA for rearranged Ig kappa light chain variable region
(1-370)
ACCESSION X72441
NID 941350
KEYWORDS immunoglobulin; J-segment; kappa light chain; V-region.
SOURCE Human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 370)
AUTHORS Zachau, H.G.
TITLE Direct Submission
JOURNAL Submitted (26-APP-1993) H.G. Zachau, Institut fuer Physiologische Chemie, der Universitaet Muenchen, Schillerstr 44, 8050 Muenchen 2, FRG

[illegible]

ORIGIN

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 Best Local Similarity 92.4%; Pred. No. 1.55e-221;
 Matches 291; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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 Qy 4 GAGCTACCCAGCTCCATGTCCTCTCTGTCATTTGNGAGACAGAGTCACATCACT 63
 Db 61 tgcggcgaagtcagagcattagcagctatttaaatgggtatcagcagaaacaggagaa 120
 Qy 64 TCGCGGCAAGTCAGATATTAGCAGAACTTAAATGGTATCAGCAGAAACAGGGACA 123
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 Qy 124 GCCCCTAAGGTCCTGATCTATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCGAGGTC 183
 Db 181 agtgcagtgatctgagacagatttccactctcaccatcagcagctctgcaacctgaagt 240
 Qy 184 AGTGCAGTGGATCTGGACAGATTTCCACTCTCACCATCACCAGTCTGCAACCTGAAGAT 243
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 Db 301 aagctggagatcaaa 315
 Qy 304 AAGGTGGAAGTCAAA 318

RESULT 13 HUMIGHY 326 bp mRNA PRI 09-NOV-1994
 LOCUS Human Ig rearranged gamma-chain mRNA V-region, partial cds.
 DEFINITION L03160
 ACCESSION g185395
 NID
 KEYWORDS V-region; immunoglobulin gamma-chain; immunoglobulin heavy chain; processed gene.
 SOURCE Homo sapiens (tissue library: BMHIV) adult bone marrow cDNA to mRNA.

ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 326)
 AUTHORS Collet, T.A., Roben, P., O'Kennedy, R., Barbas, C.F. III., Burton, D.R. and Lerner, R.A.
 TITLE A binary plasmid system for shuffling combinatorial antibody libraries
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
 MEDLINE 93066172
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 BASE COUNT 86 a 88 c 76 g 76 t
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Query Match 84.5%; Score 268; DB 99; Length 326;

Best Local Similarity 92.4%; Pred. No. 1.55e-221; Indels 0; Gaps 0;
 Matches 291; Conservative 0; Mismatches 24;

Db 1 gagctaccagctccatccctcctctctgcatctgttagagacagagtcaccatcact 60
 Qy 4 GAGCTACCCAGCTCCATGTCCTCTCTGTCATTTGNGAGACAGAGTCACATCACT 63
 Db 61 tgcggcgaagtcagagcattagcagctatttaaatgggtatcagcagaaacaggagaa 120
 Qy 64 TCGCGGCAAGTCAGATATTAGCAGAACTTAAATGGTATCAGCAGAAACAGGGACA 123
 Db 121 gccctaaagctcctgctatctgtgcatccagtttgcaaaagtggtcccatcaaggttc 180
 Qy 124 GCCCCTAAGGTCCTGATCTATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCGAGGTC 183
 Db 181 agtgcagtgatctgagacagatttccactctcaccatcagcagctctgcaacctgaagt 240
 Qy 184 AGTGCAGTGGATCTGGACAGATTTCCACTCTCACCATCACCAGTCTGCAACCTGAAGAT 243
 Db 241 ttgcaactactactctcaacagagttacagttaccccgctacacttttgccaggggacc 300
 Qy 244 TTTGCAACTTACTATTGCAACAGAGTTACACAACCCCTCGAGGTTGGGCCAAGGGACC 303
 Db 301 aagctggagatcaaa 315
 Qy 304 AAGGTGGAAGTCAAA 318

RESULT 14 HSGVVKC47 348 bp DNA PRI 19-OCT-1995
 LOCUS H.sapiens rearranged immunoglobulin kappa light chain V-region (VK-1).
 ACCESSION Z37334
 NID 9587329
 KEYWORDS immunoglobulin kappa chain: variable region.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates, Catarrhini, Homidae, Homo.
 REFERENCE 1 (bases 1 to 348)
 AUTHORS WELSCHEF, M.

TITLE Direct Submission
 JOURNAL Submitted (01-SEP-1994) M.Weischof, University of Heidelberg, Institute of Immunology, Dept. of Transplantation Immunology, Im Neuenheimer Feld 305 69120 Heidelberg, Germany
 REFERENCE 2 (bases 1 to 348)
 AUTHORS WELSCHEF, M., TERPES, P., Kolbinger, F., ZEW, M., DUEBEL, S., POPPSAM, H., Hain, C., FINGER, M., Jung, M., Moldenhauer, G., Hayashi, N., Little, M. and OPELZ, G.

TITLE Amino acid sequence based PCR primers for amplification of rearranged human heavy and light chain immunoglobulin variable region genes
 JOURNAL J. Immunol. Methods 179 (2), 203-214 (1995)

JOURNAL 95181824 Location/Qualifiers
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QY	190	AGTGGATCTGGGAAGATTTCTATCAATATCAATCAATCTGCTAAATCTGAARA	249
Db	241	acttaactcgtcaacagagattacatacaacccgttgagacgttcggccaaaggagacaaagta	300
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Db	301	gaaatcaaa	309
QY	310	GAACTCAA	318

RESULT	10
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DEFINITION	H.sapiens mRNA for Ig light chain, variable region (ID:U0039VL).
ACCESSION	X84343
NID	g791023
KEYWORDS	immunoglobulin light chain variable region.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata, Eutheria, Primates, Catarrhini, Hominoidea, Homo.
AUTHORS	1 (bases 1 to 322) Hashimoto, S., Domo, M., Wakai, M., Allen, S. L., Lichtman, S. M., Schulman, P., Vinciguerra, V. P., Ferrarini, M., Silver, J., and Chiorazzi, N.
TITLE	Somatic diversification and selection of immunoglobulin heavy and light chain variable region genes in IgG+ CD5+ chronic lymphocytic leukemia B cells
JOURNAL	J. Exp. Med. 181 (4), 1507-1517 (1995)
MEDLINE	95213674
REFERENCE	2 (bases 1 to 322)
AUTHORS	Chiorazzi, N.
TITLE	Direct Submission
JOURNAL	Submitted (01-FEB-1995) N. Chiorazzi, North Shore University Hospital, Cornell University Medical College, 300 Community Drive, Manhasset, New York 11030, USA
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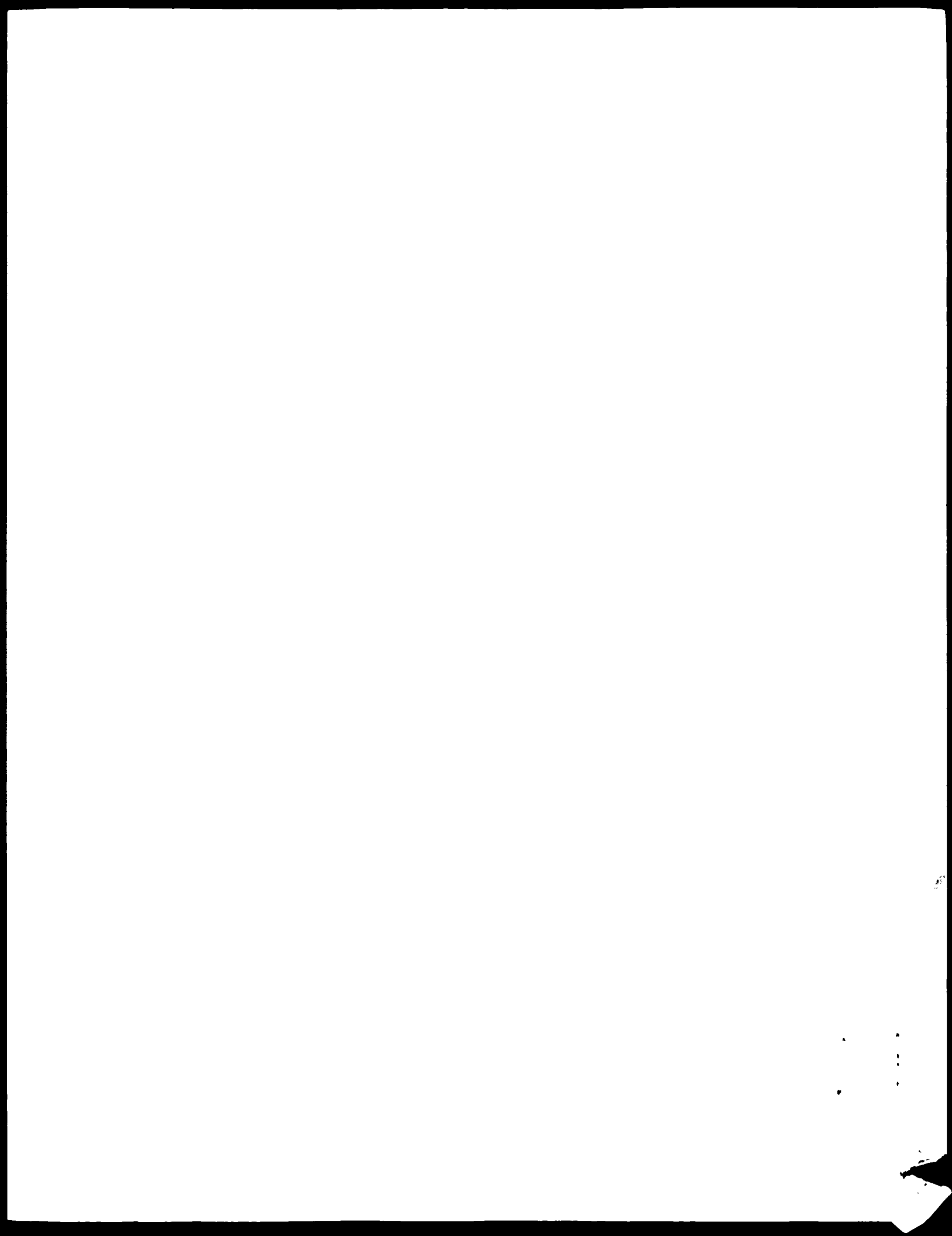
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RESULT 15 E07633 333 bp RNA PAT 26-NOV-1996
 LOCUS
 DEFINITION DNA encoding VL region of human monoclonal antibody that specifically acts against lung cancer cell, breast cancer cell, stomach cancer cell and colon cancer cell, but not against normal fibroblast.
 ACCESSION E07633
 NID Q2175758
 KEYWORDS JP 1994153984-A/2.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Vertebrate; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.
 1 (bases 1 to 333)
 Hironori M. and Katsumi M.
 ANTIBODY AND ANTIBODY CDNA
 Patent: JP 1994153984-A 2 03-JUN-1994;
 MORINAGA & CO LTD
 OS Homo sapiens (human)
 PN JP 1994153984-A/2
 PD 03-JUN-1994
 PF 27-NOV-1992 JP 1992318702
 PI MURAKAMI HIRONORI, MOCHIZUKI KATSUMI
 PC C12F21/08.A51K49/395.A61K29/395.C12N5/24.C12N15/07.C12N15/13.
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Search completed: Tue Feb 24 08:59:39 1998
 Job time : 436 secs.



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Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Pyder,S.E., Scott,J.L., Saudek,D.M., Shirley,P.,
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He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.P., Posen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280

CONTACT: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse

FEATURES
source
Location/Qualifiers
1..341

/organism="Homo sapiens"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/clone_lib="Pancreas tumor I"
/dev_stage="adult"
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BASE COUNT
ORIGIN
74 a 79 c 100 g 83 t 5 others

Query Match 32.8%; Score 122; DB 25; Length 341;
Best Local Similarity 81.5%; Pred. No. 3.25e-195;
Matches 154; Conservative 0; Mismatches 35; Indels 0; Gaps 0.
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Qy 10a gttccgcagcccccagccagggggtggagtggtggcaggttatctctatnaccgtag 167
|||||
Db 159 tcaacaatatatgcagattccgtgaaggccgattcatctccagagacgattccaa 218
|||||
Qy 168 TAATCAATACATTACAGACTCCGTGAAGGGCCGATTACCGCTCTCCAGAGACAATTCGAG 227
|||||
Db 219 gaacacagctctttgtgcaatnaacagcgtgagcattctgaggacacaggggtctttatg 278
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Qy 22a CAACAGCGTCTTCTCCAAATGACACAGCTGACACCGGAGGACACCGCTCTCTATTACTG 287
|||||
Db 279 tgtcagaga 297
|||||
Qy 288 TCGGACAGA 296

RESULT 2
LOCUS AA360289 240 bp mRNA EST 21-APR-1997
DEFINITION EST59410 Lymph node, subtracted Homo sapiens cDNA 5' end similar to
similar to immunoglobulin gamma heavy chain, V(H)1 region
(GB:U03894).
ACCESSION AA360289
NID Q2012607
KEYWORDS EST:
SOURCE human.

ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 240)

AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse

FEATURES

source

Location/Qualifiers

1..240

/organism="Homo sapiens"

/note="Organ: lymph node; Vector: pBluescript SK-; Site_1:

ECORI; Site_2: XhoI"

/clone_lib="Lymph node, subtracted"

/dev_stage="adult"

<1..>240

BASE COUNT 64 a 56 c 66 g 53 t 1 others

ORIGIN

Query Match 32.3%; Score 120; DB 50; Length 240;

Best Local Similarity 75.8%; Pred. No. 4.92e-191;

Matches 182; Conservative 0; Mismatches 57; Indels 1; Gaps 1;

Db 1 aagggggctgggtggtttctacattagatgtagtagtagtagtagtagtagtagtagtag 60

|||||

Qy 127 AAGGGGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 186

|||||

Db 61 tctgtgaaggagccgattccacattctccagagacacgacgacgacgacgacgacgacgacg 120

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Qy 187 TCGTGAAGGGCGGATTCACCGCTCTCCAGAGACAATTCGAGAGACAATTCGAGAGACA 246

|||||

Db 121 atgaacagcctgacagccgacgacgacgacgacgacgacgacgacgacgacgacgacgacg 180

|||||

Qy 247 ATGAACAGCCTGAGACCCGAGGAGACACCGCTCTCCAGAGACAATTCGAGAGACA 306

|||||

Db 181 agcagagcgtggtctaggtagtagtagtagtagtagtagtagtagtagtagtagtagtag 240

|||||

Qy 307 GATATGSAATAAGGGGGGATTAACCTTGAAGAAAT-GGGGGTCAGGAAATTAATTAAT 365

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RESULT 3

LOCUS AA326955 280 bp mRNA EST 20-APR-1997

DEFINITION EST30467 Colon I Homo sapiens cDNA 5' end similar to immunoglobulin

mu heavy chain, VDJC regions.

ACCESSION AA326955

NID g1979434

KEYWORDS EST:

SOURCE human.

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ACCESSION	AA352777				
NID	g2005188				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 267)				
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.H., Lev,N.H., Kirkness,E.F., Weinstock,K.G., Gage,J.D., White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C., Clayton,R.A., Cline,T.K., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Flytzgerald,L.M., Fitzhugh,W.M., Frithman,J.L., Geoghagen,N.S., Glodek,A., Gnani,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,F.P., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Teterback,T.P., Weidman,J.F., Willy,Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,F.J., Dinke,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hodson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,I., Wei,Y.F., Wung,J., Xu,S., Yu,C.L., Ruben,S.M., Dillion,P.J., Pannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.				
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence				
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)				
MEDLINE	98026280				
COMMENT	Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 2712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse. Location/Qualifiers 1..267 /organism="Homo sapiens" /vector="Vector; paluescript SK-"; Site_1: EORI; Site_2: XhoI" /clone_lib="Activated T-cells XX" /cell_type="T-lymphocyte" /dev_stage="adult" ^-1 ^267 61 a 54 c 79 g 70 t 3 others mpna BASE COUNT ORIGIN Query Match 14.5%; Score 54; DB 76; Length 267; Best Local Similarity 84.6%; Pred.No. 1,13e-58; Matches 66; Conservative 0; Mismatches 12; Indels 0; Gaps 0; Db 104 gaggtacggcccggtggagtcctggggaggcctgtatcacagcctggcgcagtccctgaactc 163 QY 1 GAAGTGACGCTGTCTGAATCTAGGAGGAGCGGTGGTTGATAGCTTAGGAGAGAGGTCCTCAAGAC 60 Db 164 taattgtcagcgcctctaga 181 - QY 61 TCCTGTGCAGCGCTGTGGA 78 RESULT 11 LOCUS AA377074 291 bp mRNA EST 21-APR-1997 DEFINITION EST69603 Small intestine I Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, VDJ regions (AF014165). ACCESSION AA377074 NID g2029413				



Contract: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

```

FEATURES
  source
    Location/Qualifiers
      1..209
        /organism="Homo sapiens"

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```

      mRNA      43 a      62 c      48 g      55 t      1 others
BASE COUNT
ORIGIN

Query Match      13.7%      Score 61: DB 58: Length 209:
Best Local Similarity 63.9%      Pred. No. 5,23a-53:
Matches 119: Conservative 0: Mismatches 59: Indels 0: Gaps 0:

Db      2 gaattttttccctgggaataatctgactacacccctgggaactctgtgtaattttttgtttacc 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp      225 gaaattgtctgggaacggcgaatcgcccttttcaaggagcicgaattattgatttact 166
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      62 attgcagacttgatcacatccatcaccaacacactttgttcggggagcctgacacacca 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp      165 tccatcaaacatataatctccacacacacacacacacacacacacacacacacacacacac 106
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      182 cccacact 189
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp      45 cccagagc 38
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RESULT 12      T27727      299 bp      mRNA      EST      06-SEP-1995
LOCUS      EST113874 Homo sapiens cDNA 5' end similar to immunoglobulin mu
DEFINITION      (gamma) heavy chain, V(I)DJC regions (H1:3057).
ACCESSION      T27727
NID      g609825
KEYWORDS      EST.
SOURCE      human primer-M13 Reverse library-Human Testis.
ORGANISM      Homo sapiens
Eukaryote: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE      1 (bases 1 to 299)
AUTHORS      Adams M.D., Kertavagge A.P., Fleischmann R.D., Fuldner R.A.,
      Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
      White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
      Clayton R.A., Cline P.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
      Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geodhagen N.S.M.,
      Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle J.P.S.,
      Kelley J.M., Kline K.M., Kelley J.C., Lin L.I., Marmaros S.M.,
      Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T.,
      Pellegriano S.M., Phillips C.A., Pyder S.E., Scott J.L.,
      Saudex D.M., Shirley P., Small K.V., Spriggs T.A., Utterback T.P.,
      Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
      Coleman T.A., Collins E.J., Dinke D., Feng P., Ferrie A.,
      Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
      Gruber J., Hudson P., Kim A., Kozak R., Kunsch J., Li H.,
      Messner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C.,
      Yu G.-T., Rubin S.M., Dillon P., Fannon M.P., Rosen C.A.,
      Haseltine W.A., Fields C., Fraser C.M., and Venter J.C.
      Initial Assessment of Human Gene Diversity and Expression Patterns
      Based Upon 52 Million Basepairs of cDNA Sequence
      Unpublished (1995)
Contact: Venter, J.C.
The Institute for Genomic Research
932 Cliffer Rd. Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)

FEATURES
Source      1..299
            /organism="Homo sapiens"
mRNA      1..299
BASE COUNT      62 a      77 c      95 g      60 t      3 others
ORIGIN

Query Match      13.2%      Score 49: DB 59: Length 287:
Best Local Similarity 66.2%      Pred. No. 2,49a-49:
Matches 119: Conservative 0: Mismatches 45: Indels 0: Gaps 0:

Db      80 agttcagctacagagtcagagcccgagagactgagagagcttcgagagacccctgaccca 149
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Cp      2 aggttcagctacagagtcagagcccgagagactgagagagcttcgagagacccctgaccca 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Cp      62 cctgttcagcagcctctcagattccaccttcactgctgttatgctgacacacaccc 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      200 cagggaagggactgcagctg 219
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Cp      122 cagggaagggactgcagctg 141
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RESULT 13      T27609      287 bp      mRNA      EST      06-SEP-1995
LOCUS      EST1101034 Homo sapiens cDNA 5' end similar to immunoglobulin mu
DEFINITION      heavy chain, VDJC regions (GB:M18512) (H1:3056).
ACCESSION      T27609
NID      g609707
KEYWORDS      EST.
SOURCE      human primer-M13 Reverse library-Human Pancreas.
ORGANISM      Homo sapiens
Eukaryote: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE      1 (bases 1 to 287)
AUTHORS      Adams M.D., Kertavagge A.P., Fleischmann R.D., Fuldner R.A.,
      Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
      White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
      Clayton R.A., Cline P.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
      Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geodhagen N.S.M.,
      Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle J.P.S.,
      Kelley J.M., Kline K.M., Kelley J.C., Lin L.I., Marmaros S.M.,
      Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T.,
      Pellegriano S.M., Phillips C.A., Pyder S.E., Scott J.L.,
      Saudex D.M., Shirley P., Small K.V., Spriggs T.A., Utterback T.P.,
      Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
      Coleman T.A., Collins E.J., Dinke D., Feng P., Ferrie A.,
      Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
      Gruber J., Hudson P., Kim A., Kozak R., Kunsch J., Li H.,
      Messner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C.,
      Yu G.-T., Rubin S.M., Dillon P., Fannon M.P., Rosen C.A.,
      Haseltine W.A., Fields C., Fraser C.M., and Venter J.C.
      Initial Assessment of Human Gene Diversity and Expression Patterns
      Based Upon 52 Million Basepairs of cDNA Sequence
      Unpublished (1995)
Contact: Venter, J.C.
The Institute for Genomic Research
932 Cliffer Rd. Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)

FEATURES
Source      1..287
            /organism="Homo sapiens"
mRNA      1..287
BASE COUNT      62 a      77 c      95 g      60 t      3 others
ORIGIN

Query Match      13.2%      Score 49: DB 59: Length 287:
Best Local Similarity 66.2%      Pred. No. 2,49a-49:
Matches 119: Conservative 0: Mismatches 45: Indels 0: Gaps 0:

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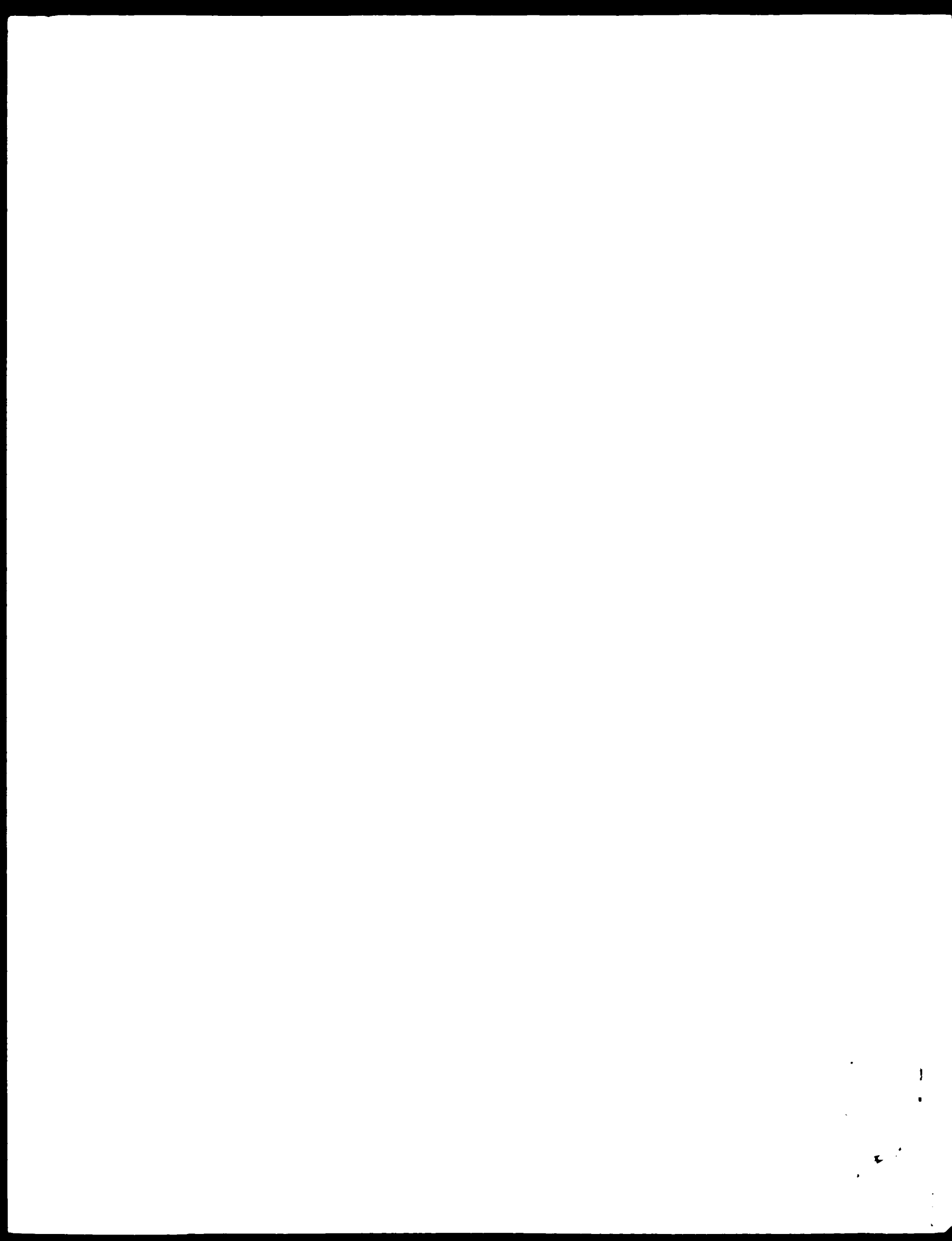

Thu Feb 26 07:04:39 1998

US-08-844-215-19.rsta

Page 9

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CC FILING DATE: 31-OCT-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/904,517
CC FILING DATE: 05-SEP-1986
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-50-7
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 576-0300
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 423 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC ORGANISM: Homo sapiens
CC CELL TYPE: Hybridoma
CC CELL LINE: PEI-1
CC FEATURE:
CC NAME/KEY: CDS
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Query Match 66.4%; Score 247; DB 6; Length 423;
Best Local Similarity 90.8%; Pred. No. 1.35e-167;
Matches 275; Conservative 0; Mismatches 28; Indels 3; Gaps 0.

Db 59 AGGTGCAGCTGGTGGAGTCTGGGGAGCGGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118
Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGAGCGGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Db 119 CTTGTGGACGCTCTGGATCTTCACCTTCAGTATGATGCTGCTGCTGCTGCTGCTGCTGCT 178
Qy 62 CTTGTGGACGCTCTGGATCTTCACCTTCAGTATGATGCTGCTGCTGCTGCTGCTGCTGCT 121

Db 179 CAGGCAAGGGCTGGAGTGGTGGAGTATCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 238
Qy 122 CAGGCAAGGGCTGGAGTGGTGGAGTATCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 181

Db 239 CAGATCTGCTGAAGGGCTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 298
Qy 182 CAGATCTGCTGAAGGGCTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 241

Db 299 TGCAATATCAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 358
Qy 242 TGCAATATCAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 301

Db 359 TTT 361
Qy 302 TTT 304

CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/458,671
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/259,372
CC FILING DATE: 14-JUN-1994
CC APPLICATION NUMBER: US 07/871,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/676,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/538,796
CC FILING DATE: 15-JUN-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/192,754
CC FILING DATE: 11-MAY-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/925,196
CC FILING DATE: 31-OCT-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/904,517
CC FILING DATE: 05-SEP-1986
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-50-7
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 576-0300
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 423 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC ORGANISM: Homo sapiens
CC CELL TYPE: Hybridoma
CC CELL LINE: PEI-1
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..423
SQ Sequence 423 BP; 87 A; 100 C; 131 G; 105 T; 0 other;

Query Match 66.4%; Score 247; DB 7; Length 423;
Best Local Similarity 90.8%; Pred. No. 1.35e-167;
Matches 275; Conservative 0; Mismatches 28; Indels 0; Gaps 0.

Db 59 AGGTGCAGCTGGTGGAGTCTGGGGAGCGGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118
Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGAGCGGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Db 119 CTTGTGGACGCTCTGGATCTTCACCTTCAGTATGATGCTGCTGCTGCTGCTGCTGCTGCT 178
Qy 62 CTTGTGGACGCTCTGGATCTTCACCTTCAGTATGATGCTGCTGCTGCTGCTGCTGCTGCT 121

Db 179 CAGGCAAGGGCTGGAGTGGTGGAGTATCATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 238

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 47:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 294 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC IMMEDIATE SOURCE:
CC CLONE: VR25C
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..294
SQ Sequence 294 BP: 53 A: 71 C: 96 G: 64 T: 0 other:

Query Match 55.9% Score 208: DB 11: Length 294:
Best Local Similarity 85.6% Pred No 1.98e-137:
Matches 250: Conservative 0: Mismatches 42: Indels 0: Gaps 0:

Db 1 GAGGTGCAGCTGTTGGAGTCTGGGGAGAGGCTTGGTACAGAGGCTGGGGAGGCTGGAGACTC 60
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QY 1 GAGGTGCAGCTGTTGGAGTCTGGGGAGAGGCTTGGTACAGAGGCTGGGGAGGCTGGAGACTC 60
Db 61 TCGTGTGCAGGCTGCTGATACACCTTACAGCTATGAGCTATGAGCTATGAGCTATGAGCTAT 120
|||||
QY 61 TCGTGTGCAGGCTGCTGATACACCTTACAGCTATGAGCTATGAGCTATGAGCTATGAGCTAT 120
Db 121 CCAGGCAAGGCGCTGGAGGCGGTGGCAGGTATATGAGTATGAGTATGAGTATGAGTATGAG 180
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QY 121 CCAGGCAAGGCGCTGGAGGCGGTGGCAGGTATATGAGTATGAGTATGAGTATGAGTATGAG 180
Db 181 GAGAGATGCGTGAAGGCGGTGGCAGGTATATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 240
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QY 181 GAGAGATGCGTGAAGGCGGTGGCAGGTATATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 240
Db 241 CTGCAATATGAGAGGCTGAGAGGAG 292
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QY 241 CTGCAATATGAGAGGCTGAGAGGAG 292

RESULT 7
ID PCT-US93-10555-4: STANDARD: DNA: UNC: 345 BP
AC xxxxxx
DT 01-JAN-1900
DE Sequence 43: Application PC/TUS9310555
CC Sequence 43: Application PC/TUS9310555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
THROUGH
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGA
TES
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1890 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: PD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 41:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 345 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC IMMEDIATE SOURCE:
CC CLONE: SP41-29
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CC NAME/KEY: CDS
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RESULT 8
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DT 01-JAN-1900
DE Sequence 43: Application PC/TUS9310555
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CC CLASSIFICATION:


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CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC IMMEDIATE SOURCE:
CC CLONE: SpA3-37
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CC LOCATION: 1..360
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Query Match      52.2%; Score 194; DB 11; Length 360;
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Search completed: Tue Feb 24 14:30:27 1998
Job time : 60 secs.

WATERMAN

(TM)

Release 2.15, Feb. 9, 1995, Bioinformatics Research Unit
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MPSrchEng v.1.1 - C.A. Database search, using Smith-Waterman algorithm
Pub on: Tue Feb 24 09:40:37 1998, Maspar time 62.95 Seconds
Tabular output not generated.

Title: >US-08-844-215-19
Description: (1372) from US0884215.seq
Perfect Score: 372
N A. Sequence: 1 CAGGTCCAGTCCGTCGACTG
Comp: CCGCTGGTCACGTCCTGCTCA 372
CCTCATCTCTGACGACTGACG
Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0
Searched: 159651 seqs, 57698962 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq30
1:part2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.102; Variance 4.826; scale 1.679
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result	No.	Score	Query Match	Length	Description	Pred. No.	
1	263	70.7	593	13	Human immunoglobulin	5.69e-163	
2	257	69.1	345	33	Anti-TGF beta-2 scfv	1.01e-158	
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4	253	68.0	344	33	Anti-TGF beta-1 scfv	6.82e-156	
5	250	67.2	359	33	Anti-TGF beta-1 scfv	9.34e-154	
6	249	66.9	121	2	Peptides heavy chain v	4.66e-153	
7	247	66.4	423	33	Monoclonal antibody p	1.19e-151	
8	247	66.4	423	33	Monoclonal antibody p	1.19e-151	
9	247	66.4	439	10	Sequence of the VH re	1.19e-151	
10	247	66.4	352	7	Sequence encoding the	1.19e-151	
11	245	66.1	336	2	Anti-human Phd HAM-B	6.08e-151	
12	245	65.9	339	2	Anti-human Phd RBC-A	3.10e-150	
13	242	65.1	303	33	Anti-TGF beta-1 scfv	4.09e-148	
14	240	64.5	357	28	Coding sequence for h	1.96e-146	
15	233	64.0	356	33	Anti-TGF beta-2 scfv	2.73e-145	

16 238 54.0 357 28 T60116 Coding sequence for h 2.74e-145
17 236 53.2 342 2 Q11953 Anti-human Phd BPA-1 1.58e-143
18 234 52.9 342 2 Q11953 Anti-human Phd GAC-2 1.52e-142
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24 225 50.5 925 2 Q12816 Variable region of h 4.06e-136
25 224 50.2 357 28 T60119 Coding sequence for h 2.06e-135
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29 219 50.0 556 9 T43544 Human anti-HBs heavy 5.83e-132
30 218 50.0 456 1 Q36110 Sequence encoding Ab; 3.46e-131
31 216 50.1 375 1 Q36104 Human immunoglobulin 8.84e-130
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33 214 50.1 294 14 Q89332 CP54 VH gene. 2.27e-124
34 214 50.1 514 13 Q78961 Human immunoglobulin 2.26e-128
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39 208 50.9 519 13 Q78959 Human immunoglobulin 3.74e-124
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43 204 50.8 642 13 Q72092 Human immunoglobulin 2.42e-121
44 203 50.6 432 12 Q17171 Monoclonal antibody L 1.12e-120
45 202 50.3 582 33 T92020 DNA encoding heavy ch 5.14e-120

ALIGNMENTS

RESULT 1
ID Q78971 standard: DNA: 583 BP.
AC Q78971:
DE DE Human immunoglobulin Vh gene #33.
KW Primer: PCR: amplify: human: immunoglobulin: variable: heavy chain:
OS cosmid: placent: vector: pJH81; E.coli: mammalian: ds.
FH Key Location/Qualifiers
FT CDS 20..472
FT /product= human immunoglobulin variable heavy chain
FT /tag= a 56..167
FT /tag= b
FT /tag= c 473..475
FT /note= "miscellaneous signal, does not conform to
terminator or splice site sequence"
PN W09426895-A.
PD 24-NOV-1994. J006003.
PF 10-MAY-1993: J006003.
PR 10-MAY-1993: W0-J006003.
PA (NIBS) JAPAN TOBACCO INC.
PI Honjo T, Matsuda F;
DR WPI: 95-006791/01.
DR P-FSDB: P66323.
PT DNA fragment comprising human immunoglobulin Vh genes for the
production of human immunoglobulin in mammalian hosts
PT Claim 4: Page 72-73: (30pp) Japanese.
PS A series of genes (78971-7902) encoding human immunoglobulin variable
heavy chains. The genes were isolated and cloned from a series of cosmid
constructs: Y502, Y503, Y504, Y505, Y506, Y507, Y508, Y509, Y510, Y511,
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Y1934, Y1935, Y1936, Y1937, Y1938, Y1939, Y1940, Y1941, Y1942, Y1943,
Y1944, Y1945, Y1946, Y1947, Y1948, Y1949

CC detachment, adult respiratory distress syndrome, liver cirrhosis,
CC post myocardial infarction, post-angioplasty restenosis,

CC The fragments were ligated with ClaI-digested cosmid

CC detached

25


```

Query Match          55.98; Score 249; DB 2; Length 1521;
Best Local Similarity 87.64; Pred. No. 4,608-133;
Matches 325; Conservative 0; Mismatches 40; Indels 6; Gaps
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742 aggtgcagcgtggtggagctcggggaggcgtggtccagctgggagggtccctgagactc 801
|||||
2 AGGTCGAGCTGCTGAGCTTGGGGGAGGGGTGTCTCCAGCTGGGAGGTCCTGGAGCTCT 61
|||||
802 cctcgcagcgcctcctggagctccagctccaggagctatggcctgctgggtccggcaggctc 861
|||||
62 cctctgcacagcgtctggattcaacttcattgctccttatggcctatccattggctggcgcagctc 121
|||||

```

952 cagcgcaagggtctgtaagtgaggtggcagctatatactcctcgtgatgggaagtgatcgactcactatg 921
122 CAGGCAGGCGGCTGGAGTGGGTGGCAGGTATATGTTTTGATGGAAATTAATTAATACTATT 181
922 cagactccgtgaaggggccggaattaccatctccagagagacaattccaggggatacgctgtatg 981
182 CAGATTCGCTGTAAGTGGCGGATTTCGGCTCTCCAGAGACAATTCCAGGAACATGTTGTTTT 241
982 tgcgaatgaacacgccgagagctggagacacgcctgctgtattactgtgcgaagaagaaat 1041
242 TGCAAAATGAACAGCCTGGAGCCGAGAGACACCGGCTGCTCTATTATATGAGGATANAAGTAC 301
1042 gtatgg-tgg-ta-gttgc--tactccttgcactactggggcggagggaacctgata 1095
302 TTTTGGATGCTATTAAAGGGGGTATTATGCTGTGAAAACGGGCGTCAAGGGAATCTGATCA 361
1096 ccgtctctctca 1106
362 CCGTCTCTCTTA 372

	08-DEC-1997	(first entry)	Monoclonal antibody pbl-1 Vh region coding sequence.
			Heavy chain; light chain; variable region; human; monoclonal antibody;
			immunisation; hepatitis B virus; HBV; vaccine; mouse; fusion; xenogeneic
			peripheral blood lymphocyte; surface antigen; cell culture; ion exchange
			chromatography; size separation; antigen; primer; PCR; polymerase chain reaction
			amplification; hybridoma; infection, immunosuppression, hepatitis;
			liver transplant; ss.
			Homo sapiens.
		Key	Location/Qualifiers
		sig_peptide	1..57
		/tag= a	
		mat_peptide	58..423
		/tag= b	
		US5648077-A.	
		15-JUL-1997.	
		05-SEP-1986;	904517
		21-APR-1992;	US-871426.
		05-SEP-1986;	US-904517.
		31-OCT-1986;	US-925196.
		11-MAY-1988;	US-192754.
		15-JUN-1990;	US-538796.
		27-MAR-1991;	US-676036
		14-JUN-1994;	US-259372.
		06-JUN-1995;	US-488671.
		(SANO) SANCOC LTD.	
		Ostberg LG;	
		WPI; 97-372021/34.	
		P-PDB: W24984.	
		Treatment of hepatitis B - with human monoclonal antibody	
		Example 8; Column 15-18; 25pp; English.	
		This is the nucleotide sequence encoding the heavy chain variable (VH)	
		region from the human monoclonal antibody (MAB) pbl-1. The MAB was	
		generated by immunising humans with a hepatitis B virus (HBV) vaccine,	
		isolating peripheral blood lymphocytes (PBL) and fusing them with a	
		mouse/human xenogeneic cell line SPAN-4. Cell lines were isolated.	

CC PEI-1, ZMI-1, ZMI-2, MD3-4 and L03-3. The cell lines were then tested
 CC for production of an anti-hepatitis B virus surface antigen antibody by
 CC ELISA. The MAbs are then purified from large scale cell culture by
 CC protein A chromatography, size separation on Sepharyl S60 gel and ion
 CC exchange chromatography on Q-Sepharose. The heavy and light chains of
 CC the MAbs were isolated and their amino acid sequences determined.
 CC Primers were generated and used to amplify cDNA synthesised from RNA
 CC purified from each hybridoma cell line. The sequences of the heavy and
 CC light chains (nucleic acid and amino acid) from MAbs PEI-1, ZMI-1, ZMI-2
 CC and MD3-4 are shown in Tables 3-4 and 5-6 respectively. The MAbs can be used to
 CC treat HBV infections in immunosuppressed patients or patients with
 CC chronic active hepatitis, especially liver transplant patients.
 CC Sequence 423 BP: 87 A: 100 C: 131 G: 105 T:

Query Match 66.4% Score 247 DB 33 Length 423
 Best Local Similarity 90.8% Pred No 119e-151
 Matches 275: Conservative 0: Mismatches 28: Indels 0: Gaps 0:
 Db 59 aggtcagactgtgagcttgcagagagctggtccagctgagagctccctgagactct 118
 QY 2 AGGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 61
 Db 119 cctgtcagactgtgagcttgcagagagctggtccagctgagagctccctgagactct 178
 QY 62 CTTGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
 Db 179 cagctcagagctgtgagcttgcagagagctggtccagctgagagctccctgagactct 238
 QY 122 CAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
 Db 239 cagctcagagctgtgagcttgcagagagctggtccagctgagagctccctgagactct 298
 QY 182 CAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
 Db 299 cagctcagagctgtgagcttgcagagagctggtccagctgagagctccctgagactct 358
 QY 242 TGCAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
 Db 359 ttt 361
 QY 302 TTT 304

RESULT A
 ID T46128 standard: cDNA: 423 BP.

AC T46128.
 DT 03-MAR-1997 (first entry)
 DE Monoclonal antibody PEI-1 heavy chain variable region coding sequence.
 KW Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;
 KW xenogeneic hybridoma: SPAZ 4; PEI-1; ZMI-1; ZMI-2; MD3-4; L03-3;
 KW IgG1 class; heavy chain; light chain; variable region; ss.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT sig_peptide
 FT /*tag= a
 FT /note= "leader sequence"

PN T5556354-A.
 PD 15-OCT-1996.
 PR 05-SEP-1986: 904517.
 PR 31-OCT-1996: US-925196.
 PR 11-MAY-1988: US-192754.
 PR 15-JUN-1990: US-538796.
 PR 27-MAR-1991: US-676036.
 PR 21-APR-1992: US-974265.
 PR 14-JUN-1994: US-159972.
 PA (SANO) SANDOZ LTD.
 PI Ostberg LG.
 DR WPI: 96-476304/47.
 DR P-PSDB: W01522.

PT Human monoclonal antibodies specific for hepatitis B surface antigen
 PT are used to treat or prevent infection or in diagnostic assays.
 PS Claim 9: Column 27-28: 26pp: English.

CC Monoclonal antibodies effective for the diagnosis and treatment of
 CC diseases caused by infection with hepatitis B have been prepared from a
 CC cell line obtained by fusing a xenogeneic hybridoma designated SPAZ 4
 CC with blood cells of a patient immunised with hepatitis B vaccine.
 CC Specific antibodies are PEI-1, ZMI-1, ZMI-2, MD3-4 and L03-3, each of
 CC these being of the IgG1 class. The present sequence encodes the heavy
 CC variable chain of PEI-1.
 CC Sequence 423 BP: 87 A: 100 C: 131 G: 105 T:

Query Match 66.4% Score 247 DB 33 Length 423
 Best Local Similarity 90.8% Pred No 119e-151
 Matches 275: Conservative 0: Mismatches 28: Indels 0: Gaps 0:

Db 59 aggtcagactgtgagcttgcagagagctggtccagctgagagctccctgagactct 118
 QY 2 AGGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 61
 Db 119 cctgtcagactgtgagcttgcagagagctggtccagctgagagctccctgagactct 178
 QY 62 CTTGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
 Db 179 cagctcagagctgtgagcttgcagagagctggtccagctgagagctccctgagactct 238
 QY 122 CAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
 Db 239 cagctcagagctgtgagcttgcagagagctggtccagctgagagctccctgagactct 298
 QY 182 CAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
 Db 299 cagctcagagctgtgagcttgcagagagctggtccagctgagagctccctgagactct 358
 QY 242 TGCAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
 Db 359 ttt 361
 QY 302 TTT 304

RESULT 9

ID 064050 standard: DNA: 429 BP.

AC 064050:
 DT 08-NOV-1994 (first entry)
 DE Sequence of the VH region of monoclonal antibody PEI-1 against
 DE hepatitis B virus surface antigen.
 KW Hepatitis B virus; surface antigen; monoclonal antibody; therapy;
 KW HBSAG; diagnosis; HBV; ss.
 OS Synthetic.

FH Key Location/Qualifiers
 FT CDS
 FT /*tag= a
 FT /note= "a"

PN W09411495-A.
 PD 26-MAY-1994.
 PR 06-NOV-1992: U09749.
 PR 06-NOV-1992: W0-U09749.
 PA (SANO) SANDOZ LTD.
 PI Ostberg LG.
 DR WPI: 94-183497/22.
 DR P-PSDB: R54047.

PT Monoclonal antibodies active against Hepatitis B surface antigen
 PT - for diagnosis and treatment of Hepatitis B virus
 PS Example: Page 35: 53pp: English.
 CC Human volunteers were immunised with hepatitis B vaccine. MD3-4, ZMI-
 CC 2, ZMI-1 and PEI-1 hybridoma cell lines were derived from
 CC lymphocytes of individuals immunised with Hepatavac (Merck & Co).
 CC Antibodies PEI-1, ZMI-1, ZMI-2 and MD3-4 belong to the IgG1 class.
 CC The cell lines producing PEI-1, ZMI-1 and ZMI-2 were deposited as
 CC ATCC HB924, 913 and 912 respectively. The cell lines all behave
 CC as typical (mouse x human) x human hybridomas and produce their
 CC respective Abs in concs. ranging up to 25 mg/l in standard
 CC suspension culture. The heavy variable (VH) and light variable (LH)
 CC chains of Abs PEI-1, ZMI-1, ZMI-2 and MD3-4 were isolated and
 CC sequenced. Total RNA was extracted from 10(7) hybridoma cells
 CC of each cell line. ss DNA was synthesised using AMV-reverse

CC scarring and glomerulonephritis, also (not claimed) osteoporosis),
 CC or (ii) immune and inflammatory diseases (e.g. rheumatoid
 CC arthritis, macrophage deficiency diseases or macrophage pathogen
 CC infection). Nucleic acids encoding human antibody VH and VL can be
 CC used for prodn. of recombinant antigen-binding domains. These are
 CC highly specific, have low dissociation constants (pref. less than 5
 CC nM) and low IC50s for neutralisation.
 SQ Sequence 369 BP; 85 A; 91 C; 115 G; 78 T;
 Query Match 65.18; Score 242; DB 33; Length 369;
 Best Local Similarity 91.78; Pred. No. 4.08e-148;
 Matches 266; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 Db 2 aggtgcaactgagtgagctctggggagggcgtgctccagcctggaggtccctgagactct 61
 QY 2 AGGTGCACCT 61
 Db 62 cctgtcagccttgagctcaactctcagtagctatcaatgacactgaggtccgcagcctc 121
 QY 62 CCTGTCCAGGCTCTGAGATTACCTTTACCTGCTTATGCGATGCACTGGGTCCGCGGCTC 121
 Db 122 cagccaagggtgagtgagtggtggtgagttatcatatgagtagtgaataactatg 181
 QY 122 CAGCCAAAGGCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
 Db 182 cagactccgtgaaggcgcgtatccacatctccagagacaaatcccaagaacacgctgtatc 241
 QY 182 CAGACTCCGTGAAGGCGGCAATCACTGCTCTCCAGACAAATCCAGAGACAGCGTGTTC 241
 Db 242 tgcataatgaacagcctgagagctgagagacacgctgtgtattactgtgcg 291
 QY 242 TGCATAATGAACAGCCTGAGACTCGAGGACAGGACGCGCTGCTTACTGTGGG 291
 RESULT 14
 ID T60122 standard; cDNA; 357 BP.
 AC T60122;
 DT 15-MAY-1997 (first entry)
 DE Coding sequence for heavy chain #4.
 KW Antibody; heavy chain; light chain; variable region; human; monoclonal;
 KW complementarity determining region; human; adr type hepatitis B virus;
 KW HB virus; CDR: virus antigen; anti-HB antibody; vaccine; ss.
 OS Homo sapiens.
 PN J09020798-A.
 PD 21-JAN-1997.
 PF 11-JUL-1995; 174752.
 PR 11-JUL-1995; JF-174752.
 PA (ASAH) ASAH KASEI KOGYO KK.
 DR WPI: 97-140911/13.
 DR P-PSDB: W13927.
 PT Human anti-Hepatitis B antibody - used in a adr type HB virus
 PT vaccine
 PS Claim 10: Page 17: 20pp; Japanese.
 CC T60122-T60123 represent the coding sequences for the heavy and light
 CC chains of the human monoclonal antibody of the invention. The antibody
 CC of the invention preferably contains the sequence represented by W13912
 CC in the complementarity determining region-1 (CDR-1) of the heavy chain
 CC variable region. The antibody of the invention also contains the
 CC sequence represented by W13913 in the CDR-3 of the light chain variable
 CC region. The antibody is capable of binding to adr type hepatitis B (HB)
 CC virus antigen. A human anti-HB virus monoclonal antibody preparation
 CC which is highly safe and is effective to adr type HB virus can be
 CC provided, using the monoclonal antibody. It can also be used as a
 CC vaccine against HB infection.
 SQ Sequence 357 BP, 76 A, 89 C, 115 G, 77 T,
 Query Match 64.58; Score 240; DB 28; Length 357;
 Best Local Similarity 91.74; Pred No 1.06e-146;
 Matches 264; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 Db 7 gctggtgagctgagggagagcgtggtccagcctggggggtccctgagactctctgtgc 66
 QY 9 GCTGCTGAGCTCTGGGAGAGCGGTGCTTACCTGAGAGGTCCTGAGACTCTCTGTGC 69

Db 67 agcgtctgattcaccttcagtagtcagtgatgactgggggagcaggtccaggtcaggt 125
 QY 69 AGCGTTTGATTCACCTTCAGTGTATGTCATGTCATGTCATGTCATGTCATGTCATGTC 128
 Db 127 ggggtgaggtgggtggcacttatatgggtgagcgaactaataataattatgctgactc 186
 QY 129 GGGGCTGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 188
 Db 187 cgtggaaggccgattcacctctccagagcaatccagaacacgctgctgaggtat 246
 QY 189 CSTGAAGGGCCATTCACCTGCTCCAGAGACAAITCCAGGAACACGCTGTTTCTGCAAT 248
 Db 247 gaacacccctgagagcggagacacgctgtgtattactgtgcgagaga 294
 QY 249 GAACACCCCTGAGACCCGAGGACGACACGCGCTCTCTATTACTGTCGACAGA 296
 RESULT 15
 ID T60370 standard; DNA; 350 BP
 AC T60370;
 DT 27-NOV-1997 (first entry)
 DE Anti-TGF beta-2 scFv antibody 2A-A9 VH gene.
 KW Transforming growth factor beta-2; TGF-beta-2; human;
 KW antibody engineering; scFv; phage display; lung fibrosis;
 KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma, vascular disease, cataract, glaucoma, scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy; ss.
 OS Chimeric Homo sapiens;
 OS Chimeric synthetic.
 PN GB2305921-A.
 PD 23-APR-1997.
 PF 07-OCT-1995; 020920.
 PR 19-JAN-1995; GB-001081.
 PR 06-OCT-1995; GB-020486.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
 PI Wilton AJ;
 DR WPI: 97-215360/20.
 DR P-PSDB: W15523.
 PT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 and nucleic acid encoding
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
 PT immune and inflammatory disease
 PS Example 1: Fig 2a(ii); 184pp; English.
 CC This DNA sequence comprises the gene encoding the VH domain
 CC (W15523) of human scFv antibody 2A-A9 (also known as 11E6), which
 CC is specific for transforming growth factor (TGF) beta-2. It was
 CC isolated by panning a phage antibody library produced from cloned
 CC germline V genes and synthetic CDRs. The antigen-binding domains
 CC of human antibodies (see W15523-40) to TGF beta 1 and/or beta-2 can
 CC be used to counter the adverse effects of TGF beta, such as (i)
 CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung
 CC fibrosis, arterial injury, proliferative retinopathy, retinal
 CC detachment, adult respiratory distress syndrome, liver cirrhosis,
 CC post myocardial infarction, post-angioplasty restenosis,
 CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural
 CC scarring and glomerulonephritis, also (not claimed) osteoporosis)
 CC or (ii) immune and inflammatory diseases (e.g. rheumatoid
 CC arthritis, macrophage deficiency diseases or macrophage pathogen
 CC infection). Nucleic acids encoding human antibody VH and VI can be
 CC used for prodn. of recombinant antigen-binding domains. These are
 CC highly specific, have low dissociation constants (pref. less than 5
 CC nM) and low IC50s for neutralisation.
 SQ Sequence 350 BP; 83 A; 87 C; 108 G; 72 T;
 Query Match 64.08; Score 238; DB 33; Length 350;
 Best Local Similarity 89.98; Pred. No. 2.73e-145;



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 /cell_line="418.F3.35"
 /cell_type="B-cell, EBV-transformed and fused with
 human-mouse heterohybridoma F3B6"
 /dev_stage="adult"
 /tissue_type="peripheral blood"
 /map="14q32.33"
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 /db_xref="PID:g388022"
 /translation="LGLCWFLVALLPGVLQCVLVEGGVQVGPSPPLSCAASGF
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 LRAEDTAVYCARPVLWFRPEYNWFDWGGTIVTVSSGSASAPLTPFX"
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 /gene="IGH"
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 /codon_start=1
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 /gene="IGH"
 374..423
 /gene="IGH"
 424..454
 /gene="IGH"
 91 a 118 c 137 g 108 t

BASE COUNT
 ORIGIN

Query Match 76.1%; Score 283; DB 99; Length 454;
 Best Local Similarity 88.1%; Pred. No. 8.61e-238;
 Matches 327; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Db 53 aggtgcagctggtgagctgtggggagcgtgtgtccagccctgggaggtccctgagactct 112
 QY 2 AGGTGAGCTGTGCTGAGTGTGGGGAGAGGCTGTGCTGAGCTGTGGAGCTGTGCTG 61
 Db 113 cctgtgcagcgtgtgattccacttcagctagctatggtcagctgggtccgcaggtc 172
 QY 62 CCTGTGCAGCTGTGATTCACCTTCACGTCCTATGGCATCACCTGGGTCCGACAGCTC 121
 Db 173 caggcaaggcgtgaggtgggtggcagttatgtgtatgagtgaggaagtaataactatg 232
 QY 122 CAGGCAAGGGGCTGGAGTGGGTGGCAGGTATATGTTTGTATGGAAGTAATCAATACTATT 181
 Db 233 cagactccatgaaggccgattccaccatctccagagacaattccaaagacacgctgtatc 292
 QY 182 CACACTCCGTGACAGCGCGGATTCACCGCTCTCCAGAGACAATTCACAGAACACCGTGTTC 241
 Db 293 tgcaaatgaacacgctgagagcgcagagacacgctgtgtattactgtgcgagaccatgat 352
 QY 242 TCAAAATGAACACGCTGAGACCGCGAGCACACGCGCTGTCTATTACTGTCCGACAGAGTAC 301
 Db 353 taclatggttcaggagccctcaactcagctgttcacccctgggcccaggaacccctaatca 412
 QY 302 TTTTGTATGCATTAAAGGGGCGTACTACTCTTGAANAATGSGSGTACAGSAAACCTGTGTC 361
 Db 413 ccgtctctctca 423
 QY 362 CCCTCTCTCTCA 372

RESULT 2
 LOCUS HMTGSHQJCM 523 bp mpna PPI 06-NOV-1994
 DEFINITION Human Igh chain VDJF region mpna, partial cds
 ACCESSION L23567
 NID 9499609

KEYWORDS C-region; D-region; J-region; V-region; immunoglobulin heavy chain;
 SOURCE Homo sapiens (individual isolate Donor R) adult peripheral blood
 CDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 523)
 AUTHORS Chai, S.K., Kasalan, M.T., Ikematsu, H., Kim, M.Y. and Casali, P.
 TITLE VH-D-JH gene sequences of mAb produced by human B-1a, B-1b, and B-2
 cells
 JOURNAL Unpublished (1994)
 FEATURES Location/Qualifiers
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 106 a 138 c 161 g 118 t

SOURCE

CDS

sig_peptide

gene

V_segment

mat_peptide

D_segment

J_segment

C_region

BASE COUNT
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Query Match 72.0%; Score 258; DB 99; Length 523;
 Best Local Similarity 88.1%; Pred. No. 2.96e-233;
 Matches 327; Conservative 0; Mismatches 41; Indels 3; Gaps 3;

Db 53 aggtgcagctggtgagctgtggggagcgtgtgtccagccctgggaggtccctgagactct 112
 QY 2 AGGTGAGCTGTGCTGAGTGTGGGGAGAGGCTGTGCTGAGCTGTGGAGCTGTGCTG 61
 Db 113 cctgtgcagcgtgtgaggtccacttcacccctgggcccaggaacccctaatca 172

LEWVAVISYDGSNKYYADSVKGPFTISPONSKNTLYLQMNLSRAEDTAVYYCARGLLL

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BASE COUNT      80 a    89 c   113 g    96 t
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Query Match          71 %; Score 267; DP 95; Length 368;
Best Local Similarity 88.7%; Pred. NO. 2,75e-222;
Matches 329; Conservative 0; Mismatches 38; Indels 4; Gaps 4;

Db       2 aggtcagactggtggaaatctaggcgagacgtgggtccacctggagtggtccctgaagactct 61
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QY       2 AGGTGAGACTGCTCGANGTCTGGGGGAGGGGTGGTCACAGCTTGAGAGGTCTCTCGSACTCT 61

Db       62 cctgtgcagcctctggattcaacttcacattagctatggcatgctagggtccgccaggctc 121
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QY       62 CTTGTGCAGCGTCTGGAAITCACTTCACGTTGCTATTGGCATGCTACTGGGTCCGCCAGGCTC 121

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QY       122 CAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATGCTTTGATGSAAGTAATCAATACATAIT 181

Db       182 cagactccttgaaggcccgattcacaccatctccagagacaattccaaagaacacgcgtgctc 241
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QY       182 CAGACTCCCTGTGAAGGGCTGATTACCGCTCTCCAGAGACAATTCCAGGAAACACGCTGTCTTC 241

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QY       242 TSCAAAATGAACA3CCTGAGAACCAGAGCACGGGTGCTATTACTGTGCACAGAGGTAC 301

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QY       362 CGCTCTCCCTCA 372

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5
RESULT      S64471      399 bp      mRNA      PRI      10-JUL-1992
LOCUS      immunoglobulin heavy chain V region [human, X-linked
DEFINITION agammaglobulinemia patients, B lymphoblastoid cell lines, mRNA
PARTIAL, 399 nt].
ACCESSION  S64471
NID        Q236904
KEYWORDS
SOURCE     human B lymphoblastoid cell lines X-linked agammaglobulinemia
           patients.
ORGANISM   Homo sapiens
            Eukaryota; Euteleostomi; Chordata; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo
REFERENCE  1 (bases 1 to 399)
            Timmers, E., Kenter, M., Thompson, A., Kraakman, M.E., Berman, T.E.,
            Alt, F.W. and Schuurman, P.
AUTHORS    Diversity of immunoglobulin heavy chain gene segment rearrangement
            in B lymphoblastoid cell lines from X-linked agammaglobulinemia
            patients
JOURNAL     Eur J. Immunol. 21 (1991) 2355-2363 (1991)
MEDLINE     92008140
REMARK      Genbank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 64471] from the original journal article.
            This sequence comes from Fig.1a.
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source
gene
CDS

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Best Local Similarity 87.9%;   Pred. No. 2,560-221;
Matches 326;   Conservative 0;   Mismatches 42;   Indels 3;   Gaps 3;

Db      2 aggtcagctggtgagctctcggggagggcggtggtccagcctgagagagctgagactct 61
QY      2 AGSTGAGTGTCTGAGTCTGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 61

Db      62 cctgtgcagcgtctggattcacctctcagtagctatggcatgcactggatcctccagagctc 121
QY      62 CCGTGTGCATGTCTGTGATTACCTTACGTGCTTATAGATAGATGAGTGTGAGGAGGAGGAGG 121

Db      122 caggcaaggagctgagatgggtggcagctcatatgtagtataatgaagataataaactatg 181
QY      122 CAGGCAAGGAGCTGAGCTGGGTGGCAGGTATATGCTTTGATGCAAGTAAATCAATACATT 181

Db      182 cgaactcctgtaagggcgcgattcacctatctcagagacaaattccagacacgcgtgtatc 241
QY      182 CAGACTCTGCTAGAGGCGCGATTACCGCTCTCTCAGAGACAAATCTCAGGAACTAGGAGTTC 241

Db      242 tgcgaatgaacagcctgagagcggcagagacacggcgtgtatatactgtgcggagatagagc 301
QY      242 TGCAATGAACAGCCTGAGAGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301

Db      302 gactcac-tatagca-cgacg-tgggaatttgactactggcggcagagaaacctgagcca 358
QY      302 TTTTGGATCGAATTAGGGGGCGTTACTCTTGAAAACTGGGGGCGAGGAACTGTTGGTCA 361

Db      359 cggctctctcca 369
QY      362 CCGTCTCTCTCA 372

RESULT 6
LOCUS HUMIGHYABK 341 bp DNA PRI 03-JAN-1995
DEFINITION Human Ig germline H-chain gene V-region, clones b9-12, 33, 35,
ACCESSION M77333
NID 9185761
KEYWORDS V-region; autoantibody; germline; immunoglobulin heavy chain.
SOURCE Homo sapiens (individual isolate Baji) adult DNA.
ORGANISM Homo sapiens
Eukaryotes, mitochondrial eukaryotes, Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Glee,T., Yang,P.M., Stiminovitch,K.A., Olsen,N.T., Hillson,J.,
Wu,J., Kozin,F., Carson,D.A. and Chen,P.P.
Molecular basis of an autoantibody-associated restriction fragment
length polymorphism that confers susceptibility to autoimmune
diseases
JOURNAL 7. Clin Invest 88 (1), 193-203 (1991)
MEDLINE 91277280
FEATURES
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intron

gene

cns

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Best Local Similarity 94.9%; Pred No 2 37e-220;
Matches 280; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy 242 tcaataaagcgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 295
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RESULT 9 HUMIGHYAAS 360 bp DNA PRI 03-JAN-1995
LOCUS Human Ig germline H-chain gene V-region, clone Nov.
DEFINITION M77315
ACCESSION 9185726
NID
KEYWORDS V-region; autoantibody; germline; immunoglobulin heavy chain.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 360)
AUTHORS Olee,T., Yang,P.M., Siminovich,K.A., Olsen,N.J., Hillson,J., Wu,J., Korin,F., Carson,D.A. and Chen,P.P.
TITLE Molecular basis of an autoantibody-associated restriction fragment length polymorphism that confers susceptibility to autoimmune diseases
JOURNAL J Clin. Invest. 88 (1), 193-203 (1991)
MEDLINE 91277280
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        /db_xref="PID:q185727"
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misc_feature 315..339
BASE COUNT 80 a 80 c 116 g 84 t
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Query Match 71.2% Score 265; DB 99; Length 360;
Best Local Similarity 94.9%; Pred No 2 37e-220;
Matches 280; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 42 aggtgcagctgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 101
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Qy 2 aggtgcagctgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 101
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Db 102 cctgtgcagctgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 161
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Qy 62 cctgtgcagctgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 121
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Db 162 caggcaagggcgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 221
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Qy 122 caggcaagggcgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 181
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Db 222 cagactcgtggaagggcgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 281
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Qy 182 cagactcgtggaagggcgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 241
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Db 282 tgcataatgaacagcgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 336
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Qy 242 tgcataatgaacagcgtgagctgtggggagggcgtggccagctggggaggtccctgagactct 295
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RESULT 10 HSHAMBH 375 bp RNA PRI 10-MAR-1993
LOCUS H sapiens mRNA for HamRH heavy chain variable Ig domain.
DEFINITION X64154
ACCESSION 938353
NID
KEYWORDS heavy chain; Ig heavy chain; immunoglobulin heavy chain variable region; variable region.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 375)
AUTHORS Hughes-Jones,N.C.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-1992) N.C. Hughes-Jones, Inst of Animal Physiology and Genetics Research, Babraham Hall, Cambridge CB2 4AT, UK
REFERENCE 2 (bases 1 to 375)
AUTHORS Bye,J.M., Carter,C., Cui,Y., Gorlick,P.D., Songsivilai,S., Winter,G., Hughes-Jones,N.C. and Marks,J.D.
TITLE Germine variable region gene segment derivation of human monoclonal anti-Rh(D) antibodies. Evidence for affinity maturation by somatic hypermutation and repertoire shift
J Clin Invest. 90 (6), 2491-2499 (1992)
MEDLINE 93107334
COMMENT See also X64148-69.
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KEYWORDS
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ORGANISM    Homo sapiens
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AUTHORS     Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE       1 (bases 1 to 375)
JOURNAL     Glas, A.M., Nottenburg, C. and Milner, E.C.
MEDLINE     Analysis of rearranged immunoglobulin heavy chain variable region
AUTHORS     genes obtained from a bone marrow transplant (BMT) recipient
TITLE       Clin. Exp. Immunol. 107 (2), 372-380 (1997)
JOURNAL     97182739
MEDLINE     2 (bases 1 to 375)
AUTHORS     Glas, A.M., Nottenburg, C. and Milner, E.C.B.
TITLE       Direct Submission
JOURNAL     Submitted (26-Nov-1996) Immunology, Virginia Mason Research Center,
            1000 Seneca Street, Seattle, WA 98101, USA
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Query Match 71.2%; Score 265, DB 95, Length 375;
Best Local Similarity 87.4%; Pred. No. 2,37e-220;
Matches 327; Conservative 0; Mismatches 44; Indels 3; Gaps 2;

Db 2 aggtgcagctgtgagctctggggagagcgtggtccagcctggagctccctgagactct 61
QY 2 AGGTGCAGCTGTGAGCTCTGGGGAGAGCGTGTCCAGCCTGGAGCTCCCTGAGACTCT 61

Db 62 cctgtgcagcctctgattccacttcagtagctatggcctacactgggtccgcaggctc 121
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Db 122 caggcaagggtctgagtggtggcagtgatcatatcatatgatggaagtaataatactatg 181
QY 122 CAGGCAAGGCTCTGAGTGGTGGCAGTGATCATATCATATGATGGAAGTAATAACTATG 181

Db 182 cagactcctgaaggcagcagctacacatctccacagacaaatccacagacacagctatgc 241
QY 182 CAGACTCCTGAAGGCAGCAGCTACACATCTCCACAGACAAATCCACAGACACAGCTATGC 241

Db 242 tgcacatgacacagcctgagagcagcagcagcagcagcagcagcagcagcagcagcagc 301
QY 242 TGCACATGACACAGCCTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 301

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Db 362 tcacagctctctcca 375
QY 369 TCACCGCTCTCTCA 372

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RESULT 13
LOCUS      HSRUP94H 384 bp RNA PRI 28-OCT-1994
DEFINITION Homo sapiens mRNA for anti-Sm antibody VH chain (VH3/JH6/JH5).
ACCESSION Z46379
KEYWORDS   g587147
            anti-Sm antibody; diversity region; immunoglobulin heavy chain;
            joining region; variable region.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE  1 (bases 1 to 384)
AUTHORS     Mahmoudi, M., Edwards, J., Cairns, E. and Bell, D.
TITLE       Molecular characterization of natural human anti-Sm autoantibodies
JOURNAL     Unpublished
REFERENCE  2 (bases 1 to 384)
AUTHORS     Mahmoudi, M.
TITLE       Direct Submission
JOURNAL     Submitted (24-OCT-1994) Mahmoudi M., University of Western Ontario,
            Medicine and Microbiology and Immunology, University Hospital Room
            BBE-12, London, Ontario, Canada, N6A 5A5
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SOURCE      Location/Qualifiers
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            /note="Author-given protein sequence is in conflict with
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            /db_xref="PID:g1340168"
            /translation="QVQLVESGGGVQPGSLRFLSCAASGFTFSYGMHWVQAPGKG
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            YDSSGYYYYVYGMVWGQGLTVVSS"
BASE COUNT  91 a 88 c 116 g 89 t
ORIGIN
Query Match 71.2%; Score 265, DB 90, Length 384;
Best Local Similarity 94.9%; Pred. No. 2,37e-220;
Matches 280; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 2 aggtgcagcctggtgagctctggggagagcgtggtccagcctggagctccctgagactct 61
QY 2 AGGTGCAGCTGTGAGCTCTGGGGAGAGCGTGTCCAGCCTGGAGCTCCCTGAGACTCT 61

Db 62 cctgtgcagcctctggtgattccacttcagtagctatggcctacactgggtccgcaggctc 121
QY 62 CCTGTGCAGCCTCTGATTCCACTTCAGTAGCTATGGCCTACACTGGGTCCGCAGGCTC 121

Db 122 cagcacaagggtctgagtggtggcagtgatcatatgatggaagtaataataactatg 181
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Db 182 cagactcctgaaggcagcagctacacatctccacagacaaatccacagacacagcagcagcagc 241
QY 182 CAGACTCCTGAAGGCAGCAGCTACACATCTCCACAGACAAATCCACAGACACAGCTCTTC 241

Db 242 tgcacatgacacagcctgagagcagcagcagcagcagcagcagcagcagcagcagcagc 296

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1

CC further information Trace considered overall poor quality Seq
CC primer: -28m13 rev2 ET from Amersham High quality sequence stop: 1.
FH Key Location/Qualifiers
FT source
FT 1..400
FT /organism="Homo sapiens"
FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a
FT modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer [5'
FT TGTTACCAATCTGAAGTGGAGCGCGCGTCTTTTCTTTTCTTTT 3']
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT73 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M. Fatima Bonaldo."
FT /clone="770541"
FT /sex="Female"
FT /clone.lib="Soares ovary tumor NBH0T"
FT /tissue_type="Ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
FT <1..>400
FT mRNA
SQ Sequence 400 BP; 90 A; 120 C; 106 G; 84 T; 0 other.

Query Match 59 7%; Score 188; DB 60; Length 400;
Best Local Similarity 83 3%; Pred No 0.00e+00;
Matches 260; Conservative 0; Mismatches 48; Indels 4; Gaps 3;
Db 70 acgagctccagggaccctgttctgtctccaggggaagagccacctctctgcagg 129
QY 7 ACCGAGCTCCACGACCGCTGTGTGTCTCCAGGGGAAGAGCCCTCTCTGCAGG 66
Db 130 gccagtcacagtgtagcagcagctgttagcctgtgtaccagcagaacacctgcccagct 189
QY 67 GCCAGTCACAGTGTGGTAACAA-T--TTAGCTTGTGTATGAGTGAAGAACCTGTGGCAGGCT 123
Db 190 cccaggtctctctatgtgtgcattccagcaggggcaactggcctcccccagacaggttcagt 249
QY 124 CCCAGGCTCTCTATTTATGCTGGAAACACACAGACGCTGTCTACCCAGACAGGTTTCACT 183
Db 250 gccagtgagctgagacagagcttcaactctcaatcggcagcagcagcagcagcagctt 309
QY 184 GCCAGT 242
Db 310 tgcagtgattactgtcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 369
QY 243 TGTAGTTATTTTGTAACTATAGTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 302
Db 370 ggtggaaatcaa 381
QY 303 GGTGAGATTCAA 314

RESULT 2
LOCUS AA515239 418 bp mRNA EST 14-JUL-1997
DEFINITION ng69c07.s1 NCI-CGAP_Lip2 Homo sapiens cDNA clone 940044 similar to
gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
ACCESSION AA515239
NID q2254839
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (bases 1 to 418)
AUTHORS NCI-CGAP.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph D
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov

Tissue Procurement: L Jeffrey Medeiros, M D ; Michael R.
Emmert-Buck, M D., Ph D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I M A G E Consortium/LLNL at:
www-bio.llnl.gov/nbrp/image/image.html

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 413.
FEATURES
source location/Qualifiers

1..418
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/note="Vector: pAMP10; mRNA made from liposarcoma, cDNA
made by oligo-dT priming Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
/clone="940044"
/clone.lib="NCI-CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
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Matches 253; Conservative 0; Mismatches 54; Indels 4; Gaps 2;

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QY 7 ACCGAGCTCCAGGACGCTGTGTGTGTCTCCAGGGGAAGAGCCCTCTCTGCAGG 66
Db 155 gccagtcacagtgtagcagcagctgttagcctgtgtaccagcagaacacctgcccagct 214
QY 67 GCCAGTCACAGTGTGGTAACAA-T--TTAGCTTGTGTATGAGTGAAGAACCTGTGGCAGGCT 123
Db 215 gccagtgagctgagacagagcttcaactctcaatcggcagcagcagcagcagcagctt 273
QY 124 CCCAGGCTCTCTATTTATGCTGGAAACACACAGACGCTGTCTACCCAGACAGGTTTCACT 183
Db 274 ggcagtgattactgtcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 333
QY 184 GCCAGT 243
Db 334 gccagtgattactgtcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 393
QY 244 GCAGTTTATTTTGTAACTATAGTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 303
Db 394 gttgaaatcaa 404
QY 304 GTCGAGATTCAA 314

RESULT 3
ID HSJ308877 standard; RNA; EST; 418 BP.
AC AA515239;
NI q2254839
DT 15-JUL-1997 (Rel. 52, Created)
ST 24-JUL-1997 (Rel 52, Last updated, Version 2)
DE ng69c07.s1 NCI-CGAP_Lip2 Homo sapiens cDNA clone 940044 similar to
gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata.
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
OC Homo.
RN [1]
RP 1-418
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP)."

COMMENT

Contact: Wilson FK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63104
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham.

FEATURES

Source
1..242
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
/clone="739953"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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BASE COUNT
OPIGIN

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Matches 192; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

Db 24 ttacgtgtatcagcagaacacctggcaggctccaggctccatctatgtgtgaccc 83
QY 91 TTAGCTTGTATCAGCAGAAACCTGGCCAGGCTCCAGGCTCCCTATTATGTGTAAC 150
Db 84 agcaggccactggcattccacagacaggttcagtgagcagtggtcgtggacagacttcaact 143
QY 151 ACCAGAGGCACTGGTACCCAGACAGAGTTCAGTGGCAGTGGTGGCAGAGAAATCACT 210
Db 144 ctacacatcatcagcagctggagctgaagatttgcagtgattactctcagcagtgatgg 203
QY 211 CTCACCAATCA-CGACCTGTCAGCTTGAGGACTTTGCGAGTTTATTTCTGTCAACACTATAG 269
Db 204 tagctcaecgctcactttcggcggaggagccacaaagtgga 242
QY 270 TACCTGGCGCTCACTTTCCGGGGGGGACCAAGGTGGA 308

RESULT 6
ID HS1258064 standard; RNA; EST; 324 BP.
AC AA464224;
NI q2189108
DT 13-JUN-1997 (Rel. 52, Created)
DT 13-JUN-1997 (Rel. 52, Last updated, Version 1)
DE zx83c06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810346
DE 5' similar to gb:M12740_cds1 IG KAPPA CHAIN PREPROMOTOP V-III REGION
KE (HUMAN):
KW EST.
OS Homo sapiens (human)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata, Euthera, Primates; Catarrhini, Hominoidea; Homo.
RN [1]
RP 1-324
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
RA Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
RA White Y., Wyllie T., Waterston R., Wilson P.;
RT "WashU-Merck EST Project 1997";

RL Unpublished.
CC Contact: Wilson FK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC est@watson.wustl.edu This clone is available royalty-free through
CC LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information Seq primer: -28m13 rev2 ET from Amersham High
CC quality sequence stop: 161.
FH Key Location/Qualifiers

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FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a
FT modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer [5',
FT TGTACCAATCTGAAGTGGAGCGGCGGTTTTTTTTTTTTTTT 3'],
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT73 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M.Fatima Bonaldo."
FT /clone="810346"
FT /sex="Female"
FT /tissue_type="ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
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Query Match 49.5%; Score 156; DB 63; Length 324;
Best Local Similarity 89.2%; Pred. No. 1.52e-258;
Matches 206; Conservative 0; Mismatches 20; Indels 5; Gaps 5;

Db 80 acgcagctctcagcagccctgtgtgtatccgggggaagccacctctctctcagg 139
QY 7 AGCGAGCTCTCAGCAGCAGCCTGTGTGTATCCAGGGAAGCCACCTCTCTCTCAGG 56
Db 140 gccagtcagagtggttagcagaacttagctgctgctacacagactctctcagcagctccc 199
QY 67 GCCAGTCAGAGTGTGGTAACTATTTAGTTGGTATATCAGCAGAAAATCTGGCAGGCTCC 126
Db 200 aggtctctctctctctgtgtgctatccacaggggagctggtatccacagcaggttcagatag 259
QY 127 AGGCTCTCTCTCTCTAT 185
Db 260 cagtgaggtctaggacagagagtgctcactcttcacattcagcagcagctcagct 310
QY 186 CAGTGGGTCTTGGGACAGAAATTAATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 232

RESULT 7
LOCUS AA464224 324 bp mRNA EST 10 JUN 1997
DEFINITION zx83c06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810346
5' similar to gb:M12740_cds1 IG KAPPA CHAIN PREPROMOTOP V-III REGION
(HUMAN):
ACCESSION AA464224
NID q2189108
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata, Mammalia; Euthera, Primates; Catarrhini, Hominoidea;
Homo.
1 (bases 1 to 324)
AUTHORS Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
White Y., Wyllie T., Waterston R., Waterston R. and Wilson R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson FK
WashU-Merck EST Project

TITLE
JOURNAL
COMMENT

modified polylinker; Site_1: Not I; Site_2: Eco RI; lstr
strand cDNA was primed with a Not I - oligo(dT) primer [5
TGTTACCAATGAAGTGAGCGCGCGGTGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNAs were size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTZ19 vector
(Pharmacia). Library constructed by Bento Soares and
M Patricia Ronaldo "
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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Sequence 244 BP; 5' A : 82 C; 60 G; 48 T; 0 other:
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Best Local Similarity 90.6%; Pred. No. 2,99e-205;
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Ddb 85 acgcagcttcacgccaccctgtctgtgctccaggaggaagcacacctcctcaggg 144
Qqy 7 ACGCAGCTTCACGCCACCCTGTGTTGTCTCCAGGAAAGACTCTCTCTCTGAGG 66
Ddb 145 gccagtcagagtgttagcaggaacttagcttgatccagcatataactgagccagagctccc 204
Qqy 67 GCCAGTCAGAGTGTGCGTAACAATTAGCTTGGTAACAGCAGAACCTCGGACAGCTCCC 126
Ddb 205 aggrctctctatctatggtgcacatccacagggcgacatgata 244
Qqy 127 AGGCTCCTCATTTATGTTGGAAACACAGAGCGCACATGGTA 166
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(HUMAN);.
ACCESSION AA464451
NID g2189335
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes, Metazoa, Chordata,
Vertebrata; Mammalia, Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 242)
AUTHORS Hillier,L., Allen,M., Howles,L., Dubouque,T., Geiseler,C., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.L.,
Moore,B., Schellenger,K., Steptoe,M., Tan,F., Thomsen,R.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE Contact: Wilton RK
JOURNAL Washington University School of Medicine
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
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organism="Homo sapiens"
/cote="Organ. ovary; Vector; pTZ19 (Pharmacia)" with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; lstr
strand cDNA was primed with a Not I - oligo(dT) primer [5
TGTTACCAATGAAGTGAGCGCGGTGGTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTZ19 vector
(Pharmacia). Library constructed by Bento Soares and
M Patricia Ronaldo "
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1..-244
Sequence 244 BP; 5' A : 82 C; 60 G; 48 T; 0 other:
Query Match 41.3%; Score 130; DB 57; Length 244;
Best Local Similarity 90.6%; Pred. No. 2,99e-205;
Matches 145; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Ddb 85 acgcagcttcacgccaccctgtctgtgctccaggaggaagcacacctcctcaggg 144
Qqy 7 ACGCAGCTTCACGCCACCCTGTGTTGTCTCCAGGAAAGACTCTCTCTCTGAGG 66
Ddb 145 gccagtcagagtgttagcaggaacttagcttgatccagcatataactgagccagagctccc 204
Qqy 67 GCCAGTCAGAGTGTGCGTAACAATTAGCTTGGTAACAGCAGAACCTCGGACAGCTCCC 126
Ddb 205 aggrctctctatctatggtgcacatccacagggcgacatgata 244
Qqy 127 AGGCTCCTCATTTATGTTGGAAACACAGAGCGCACATGGTA 166
FEATURES
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Thu Feb 26 07:04:34 1998

US-08-844-215-18.rstc

Page 9

Search completed: Tue Feb 24 08:31:31 1998
Job time : 131 secs.




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/dev_stage="adult"
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BASE COUNT
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Db      112 gccagtcagagtggttagcagcaacttagcctgggtaccagcagaacacctggccagagctccc 171
Qy      67  GCCAGTCAGAGTGTGGGTAAACAATTTAGTTTGGTATCAGGAGAAAATGGGAGAGGTC 176

Db      172 aggcctctcatctatgtgtgcattccatcagggnccactggcatccccagccaggttcagtggc 241
Qy      127  AGGCCTCTCATTTATTTGTTGTAAGACAGAGGATCTGGTATGTTGAGAGAGATTCATGAGG 186

Db      232 agtgggtctcaggacagagttcaactctccatccagcaccctggagctcagaggtttctcc 291
Qy      187  AGTGGGTCTGSSGACCAATTCATCTCCATCAATCAGTATGGTATTTGAGAGATTTGATA 246

Db      292 gtttatctatgtccagcagttataataacctgggcatcca 328
Qy      246  GTTTATCTATGTCCAGCAGTTATAATAACCTGGGCATCCA

```


The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699423
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tadb/hgi/hgi.html>)
Seq primer: M13 Reverse.

Raymond L. Wei, Y. F. Wang, J. Xu, C. Yu, G. L. Eukaryotic S.M.
Cellular, P. J. Farnham, M. P. Roesch, D. A. Huse, D. K. A. Fields, C.
Fraser, C. M. and Venter J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl): 3-174 (1995)
96026280
Other ESTs: TH0164106
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699423
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tadb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers
1..346
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/note="Organ: testis; Vector: pBluescript SK-; Site: 1;
EcoRI; Site: 2; XhoI"
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/dev_stage="adult"
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ORIGIN
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Site: 1; EcoRI; Site: 2; XhoI"
/clone_lib="Gall bladder II"
/sex="female"
/dev_stage="adult, 25 yrs"
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QY 37 CCAGGGAAGAGCCCCCCTCTCTCGCAGCCAGCCAGCTGTTACCAGAGCTCAACT 93
Db 102 gctggtatcagcaaaagccggccagagctccagagctccatctatggtgggctcagg 161
QY 94 GCTTGATATCAACAAGCTTGGCAGAGCTCCCAAGCTGCTTCATTATATGGAAGACC 153
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QY 14 CTCCAGCCACCT 73
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QY 74 AGAGATTATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 140
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Db 214 gtttggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 273
QY 191 GGTCTGGGACAGAAATTCATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 249
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RESULT 8
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DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
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to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 8
LOCUS ES13427 Testis tumor Homo sapiens cDNA 5' end similar to
DEFINITION ES13427 lymph node I Homo sapiens cDNA 5' end similar to similar
to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 405)

RESULT 10
LOCUS AA361678 283 bp mRNA EST 21-APR-1997
DEFINITION EST70993 T-cell lymphoma Homo sapiens cDNA 5' end similar to
similar to immunoglobulin kappa variable region (GR-V06640).
ACCESSION AA361678
NID 42013993
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 283)
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Feldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, F.F., Weinstock, K.G., Geyrhofer, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geohagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M.,
Phillips, C.A., Ryder, S.F., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Wiley, J.,
Rednair, D.P., Cao, L., Cepeda, M.A., Coleman, J.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S., Kim, A.K.,
Raymond, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other_ESTs: THC169243
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
7112 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/db/hgi/hgi.html>)
Seq primer: M3 Reverse
Location/Qualifiers
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Best Local Similarity 87.3% Pred. No. 5 99e-249; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Db 87 ctccagccaccctgtctgtatctccaggggaaagagccacccttctctgcagggccacatc 146
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14 ctccagccaccctgtctgtatctccaggggaaagagccacccttctctgcagggccacatc 73
Db 147 agatgtttacagaaacttgcctgtgttccatcagcaaaactgcagcagcctccagggctcc 206
|||||
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Db 207 tttctctatgtgcctccagggcagcactgtatctccagccagcagcctcagtcgcatggat 266
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Db 267 ctggagccagcaggtcact 283
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QY 194 ctggagccagcaggtcact 210
RESULT 11
LOCUS AA383914 238 bp mRNA EST 21-APR-1997
DEFINITION EST97387 Thymus II Homo sapiens cDNA 5' end similar to
immunoglobulin kappa light chain, VJ regions.
ACCESSION AA383914
NID 92036253
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 238)
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Feldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, F.F., Weinstock, K.G., Geyrhofer, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geohagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M.,
Phillips, C.A., Ryder, S.F., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Wiley, J.,
Rednair, D.P., Cao, L., Cepeda, M.A., Coleman, J.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S., Kim, A.K.,
Raymond, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other_ESTs: EST97386 THC169106
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
7112 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/db/hgi/hgi.html>)
Seq primer: M3 Reverse
Location/Qualifiers
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/dev_stage="adult, 19 yrs"
BASE COUNT 49 a 79 c 58 g 52 t
ORIGIN
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Matches 170; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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|||||
7 accagcttccagccaccctgtctgtatctccaggggaaagagccacccttctctgcagggccacatc 66
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Best Local Similarity 90.6%:   Pred. No. 1,45e-207:
Matches 145:  Conservative 0:  Mismatches 15:  Indels 0:  Gaps 0:

      85  acacagctccagagcacccctgtctgtatctccagaggaagaagccagccctctctctacaga 144
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      7  AGCAAGTATCTCAAGCAAGCCCTGTCTGTCTCAAGAGGAAAGAGCCCTGCGTATCGTAAG 166
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

      145  gccagtcagagtggttagcaggaaccttagcctggtaccagcataaacctggccaggtcccc 204
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      67  GCCAGTCAAGAGTGTGGTAAACAAATTAAGCTTGGATAGCAAGAAATGGTGTAGAGTGGG 126
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

      205  aggtccctcactgtatgtatgcctaccagagagccactagta 244
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      127  AGGCTTCCTCATTTATGTGTGAACACCAGAGACCCACTGTA 166
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15

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immunoglobulin kappa light chain, VNJ regions (GB:211894).
 A0327218
 NID
 KEYWORDS
 EST
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 Homo.
 1 (bases 1 to 289)
 Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner P.A.,
 Balt C.J., Lee N.H., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
 White O., Sutton G., Blake A., Brandon P.C., Mani-Wal, C.,
 Clayton, C.A., Cline, T.P., Cotton, M.P., Parle-Hughes J., Finch, L.D.,
 Fitzgerald, D.M., Fitzhugh W.M., Fritchman, J.L., Goodhead, N.S.,
 Glodek, A., Gnehm, C., Hanna M.C., Hedblom, P., Hinkle, S.J.,
 Kelley, J.M., Kelley, J.C., Liu, L., Marmaro, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, J.A., Nguyen, D.T., Pellierino, S.M.,
 Phillips, C.A., Pyder, S.E., Scott, J.L., Saudou, E.M., Shirley, R.,
 Small, K.V., Springs, I.A., Utterbaugh, T.R., Weidmann, R., Wiley,
 J. (bases 1 to 289)
 REFERENCE
 AUTHORS

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL *Nature* 377 (6547 Suppl.) 3-174 (1995)

KEYWORDS 96063680

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 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the tIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
 Location/Qualifiers
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BASE COUNT      66 a      88 c      73 g      59 t      3 others
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Matches 183; Conservative 0; Mismatches 32; Indels 4; Gaps 3;

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Db 131 cagggccagtcagagtggttatgagcgggtacttagccttggtaccagcagagaacccctggcca 190
Qy 63 CAGGGCCAGTCAGAGTGTCT--G-TAACAAATTAGCTTGGTATCAGCAGAAACCTGGCCA 119
Db 191 ggctcccgaggtcgtctatgagacatccagagggccactggtcattccagacaggtt 250
Qy 120 GGCTCCCGAGGCTCTCTATTATGTTGGGAAACACACAGAGCCACTGGTACCCCGAGACAGTT 179
Db 251 cagtggcagtggtgtgagacagacttcaactctcaccat 289
Qy 180 CAGTGGCAGTGGGTCTGGACAGAAATTACTCTCACCAT 218

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Search completed: Tue Feb 24 08:28:57 1998
Job time : 150 secs.

WATERMAN

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MPSrch_nu n.a. n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 08:20:59 1998. Maxpar time 192.49 seconds
Tabular output not generated.

Title: >US-08-844-215-18
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Percent Score: 915
N.A. Sequence: 1 CAGCTCAGGAGTTCAGGAGG
Comp: CTCGAGTCCAGGTCACAAATTC

Scoring table: TABLE default
Gap 5

Nmatch STD : Phase 0 Query 0

Searched: 65773 seqs, 246912998 bases x 2

Post-processing: Minimum Match 04
Listing first 45 summaries

Database: EST-A

EST1 2. EST2 3. EST3 4. EST4 5. EST5 6. EST6 7. EST7 8. EST8
9. EST9 10. EST10 11. EST11 12. EST12 13. EST13 14. EST14
15. EST15 16. EST16 17. EST17 18. EST18 19. EST19 20. EST20
21. EST21 22. EST22 23. EST23 24. EST24 25. EST25 26. EST26
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Database: EST-B

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184-EST184 185-EST185 186-EST186 187-EST187 188-EST188
189-EST189 190-EST190 191-EST191 192-EST192 193-EST193
194-EST194 195-EST195 196-EST196

Statistics: Mean 9.921; Variance 1.934; scale 5.129

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

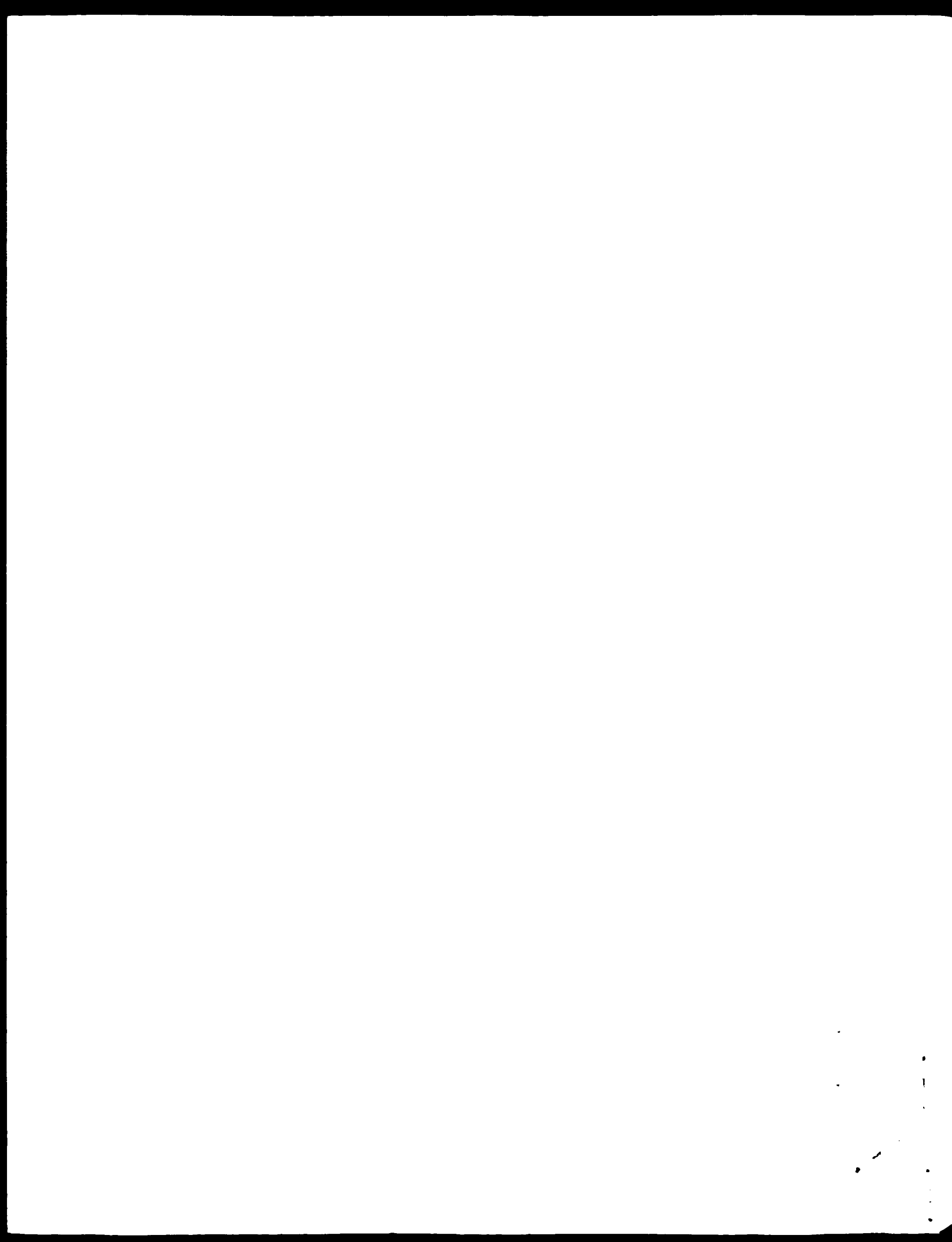
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3	175	55.6	381	58	EST69430 Homo sapiens	2.180-001
4	173	54.9	383	59	EST99871 Homo sapiens	2.500-047
5	172	54.6	332	58	EST77181 Homo sapiens	4.430-295
6	161	51.1	383	58	EST10007 Homo sapiens	5.260-272
7	141	44.8	361	28	YJ71607.11 Homo sapiens	2.530-230
8	140	44.4	570	34	YJ81008.11 Homo sapiens	3.910-228
9	136	43.2	401	40	YJ31306.11 Homo sapiens	5.790-220
10	134	42.5	360	37	YJ85601.11 Homo sapiens	7.980-216
11	133	42.2	359	64	YJ61407.11 Homo sapiens	9.170-214
12	132	41.9	282	63	YJ73512.11 Homo sapiens	1.060-211
13	131	41.6	399	59	YJ34310.11 Homo sapiens	1.270-209
14	127	40.3	385	64	YJ51905.11 Homo sapiens	2.140-201
15	127	40.3	793	58	EST10053 Homo sapiens	2.140-201
16	122	38.7	218	64	YJ65301.11 Homo sapiens	2.980-191
17	116	36.8	438	33	YJ23609.11 Homo sapiens	7.590-179
18	108	34.3	171	64	YJ47066.11 Homo sapiens	1.420-162
19	108	34.3	395	58	EST69484 Homo sapiens	1.420-162
20	108	34.3	447	89	YJ69312.11 Homo sapiens	1.420-162
21	107	34.0	151	63	YJ34005.11 Homo sapiens	1.510-160
22	103	32.7	176	81	YJ45010.11 Homo sapiens	1.840-152
23	101	32.1	516	32	YJ42011.11 Homo sapiens	1.980-148
24	98	31.1	421	27	YJ56011.11 Homo sapiens	2.120-144
25	89	28.3	210	34	YJ82031.11 Homo sapiens	1.670-124
26	89	28.3	330	45	YJ21504.11 Homo sapiens	1.970-124
27	89	28.3	434	11	YJ31108	1.970-124
28	87	27.6	279	58	EST89211 Homo sapiens	1.810-120
29	87	27.6	364	58	EST10049 Homo sapiens	1.810-120
30	86	27.3	235	55	YJ30311.11 Homo sapiens	1.750-118
31	84	26.7	488	64	YJ48005.11 Homo sapiens	1.520-114
32	83	26.3	201	64	YJ53001.11 Homo sapiens	1.420-112
33	83	26.3	470	81	YJ30011.11 Homo sapiens	1.420-112
34	81	25.7	289	58	EST100107 Homo sapiens	1.200-108
35	80	25.4	289	58	EST13441 Homo sapiens	1.090-106
36	80	25.4	503	22	YJ35009.11 Homo sapiens	1.090-106
37	76	24.1	397	28	YJ55003.11 Homo sapiens	6.950-99
38	75	23.8	261	27	YJ41403.11 Homo sapiens	6.070-97
39	74	23.5	367	2	YJ11609.11 Homo sapiens	5.260-95
40	74	23.5	387	34	YJ41609.11 Homo sapiens	5.260-95
41	74	23.5	438	34	YJ64210.11 Homo sapiens	5.260-95
42	72	22.9	120	59	YJ47100.11 Homo sapiens	3.840-91
43	68	21.6	366	64	YJ65601.11 Homo sapiens	1.920-83
44	67	21.3	199	51	YJ11410.11 Homo sapiens	1.470-81
45	67	21.3	467	64	YJ65005.11 Homo sapiens	1.470-81

ALIGNMENTS

1
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LOCUS
DEFINITION
ACCESSION
NID
KEYWORDS
SOURCE

R69532
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IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
R69532
G843049
EST
human clone=155249 library-Scores breast 2NHBst vector-p7170

01-JUN-1995



 W P S R E L H

 (TW)

Release 2 ID John F. Collins, Biocomputing Research Unit,
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MPSrch_Lnn n.a. - n.a. database search, using Smith-Waterman algorithm
 Run on: Tue Feb 24 14 18 48 1998. MacPar time: 19 79 seconds
 Tabular output not generated
 732 198 Million cell updates/sec

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 Comp: CCGAGTGGGTCAGAGGTCG CCGGTTCCAGCTCAAGTTC

Scoring table: TABLE default
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 Searched: 87931 seqs, 22995021 bases x 2
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: n-issued
 1-back: 2 51 2 52 4 53 5 54 6 55 7 56 8 PCT96 9 PCT97
 10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96
 Statistics: Mean 7.669. Variance 4 251. scale 1 804

Pred No is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred No.
1	204	64.8	812	7	US-08-053- Sequence 178	Applicat 6 725-132
2	200	63.6	900	7	US-08-053- Sequence 180	Applicat 6 089-124
3	192	61.0	900	7	US-08-053- Sequence 182	Applicat 6 646-123
4	186	59.0	325	11	PCT-US93-1 Sequence 1	Applicat 2 226-118
5	185	58.7	645	12	PCT-US94-0 Sequence 2	Applicat 1 266-117
6	185	58.7	645	13	PCT-US95-1 Sequence 2	Applicat 1 266-117
7	185	58.7	645	7	US-08-300- Sequence 2	Applicat 1 266-117
8	162	51.4	729	7	US-08-276- Sequence 157	Applicat 2 416-100
9	162	51.4	729	13	PCT-US95-0 Sequence 152	Applicat 2 416-100
10	162	51.4	729	13	PCT-US96-0 Sequence 158	Applicat 2 416-100
11	162	51.4	729	7	US-08-276- Sequence 159	Applicat 2 416-100
12	162	51.4	13254	13	US-08-276- Sequence 156	Applicat 2 416-100
13	162	51.4	13254	13	PCT-US95-0 Sequence 155	Applicat 2 416-100
14	162	51.4	13254	13	PCT-US95-0 Sequence 170	Applicat 2 416-100
15	162	51.4	13254	7	US-08-276- Sequence 170	Applicat 2 416-100
16	139	44.1	387	6	US-08-217- Sequence 1	Applicat 3 566-83
17	136	43.2	6238	1	5453363-1 Patent No 5453363	6 046-81
18	132	41.9	318	12	PCT-US94-1 Sequence 2	Applicat 5 616-78
19	132	41.9	318	11	PCT-US93-0 Sequence 3	Applicat 5 616-78

20	132	41.9	318	11	PCT-US93-0	Sequence 3	Applicatio	5 616-78
21	131	41.6	321	5	US-07-988-	Sequence 74	Applicati	3 036-77
22	131	41.6	321	5	US-08-425-	Sequence 72	Applicati	3 096-77
23	131	41.6	321	10	PCT-US92-0	Sequence 74	Applicati	3 096-77
24	131	41.6	723	5	US-07-988-	Sequence 92	Applicati	3 096-77
25	141	41.6	723	5	US-07-988-	Sequence 94	Applicati	3 096-77
26	131	41.6	723	7	US-08-425-	Sequence 89	Applicati	3 096-77
27	131	41.6	723	7	US-08-425-	Sequence 92	Applicati	3 096-77
28	131	41.6	723	10	PCT-US92-0	Sequence 92	Applicati	3 096-77
29	131	41.6	723	10	PCT-US92-0	Sequence 93	Applicati	3 096-77
30	130	41.3	381	7	US-08-487-	Sequence 82	Applicati	1 706-76
31	130	41.3	381	6	US-08-477-	Sequence 82	Applicati	1 706-76
32	130	41.3	381	5	US-07-634-	Sequence 82	Applicati	1 706-76
33	130	41.3	381	7	US-08-474-	Sequence 82	Applicati	1 706-76
34	129	41.0	360	7	US-08-201-	Sequence 62	Applicati	3 076-76
35	129	41.0	360	13	PCT-US95-1	Sequence 62	Applicati	3 076-76
36	128	40.6	1238	7	US-08-401-	Sequence 35	Applicati	5 156-75
37	128	40.6	1300	7	US-08-401-	Sequence 34	Applicati	5 156-75
38	125	39.7	312	4	US-07-789-	Sequence 7	Applicati	9 536-73
39	125	39.7	321	7	US-08-425-	Sequence 69	Applicati	9 536-73
40	125	39.7	321	5	US-07-988-	Sequence 71	Applicati	8 536-73
41	125	39.7	321	10	PCT-US92-0	Sequence 71	Applicati	8 536-73
42	125	39.7	384	5	US-08-259-	Sequence 13	Applicati	8 536-73
43	125	39.7	384	7	US-08-458-	Sequence 13	Applicati	8 536-73
44	125	39.7	847	7	US-08-053-	Sequence 184	Applicati	8 536-73
45	124	39.4	365	7	US-08-398-	Sequence 19	Applicati	4 676-72

ALIGNMENTS

RESULT 1
 ID US-08-053-131-178 STANDARD: DNA: UNC: 812 BP.
 AC XXXXXX
 DT 01-JAN-1900
 DR Sequence 178, Application US/08053131
 CC Sequence 178, Application US/08053131
 CC Patent No. 5661016
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M
 CC TITLE OF INVENTION: Transgenic N-5661016 Human Antibodies for
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 197
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Khourie and Crew
 CC STREET: One Market Plaza, Steuart Tower, Suite 200
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patented, Release #2.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER US/08/053,131
 CC FILING DATE: 26-APR-1993
 CC CLASSIFICATION: 800
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/990,860
 CC FILING DATE: 15-DEC-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/810,279
 CC FILING DATE: 17-DEC-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/853,408
 CC FILING DATE: 18-MAR-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,323
 CC REFERENCE/DOCKET NUMBER: 14643-9-3
 CC TELECOMMUNICATION INFORMATION:

CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/053.131
 CC FILING DATE: 25-APR-1993
 CC CLASSIFICATION: 800
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/490,860
 CC FILING DATE: 16-DEC-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/810,279
 CC FILING DATE: 17-DEC-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/853,408
 CC FILING DATE: 18-MAR-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-9-3
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO: 142:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 900 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: Join(116..163, 351..650)
 CC Sequence 900 bp: 220 A: 241 C: 201 G: 238 T: 0 other:

Query Match 61.0% Score 192: DB 7: Length 900:
 Best Local Similarity 86.8% Prod No 6,646-133
 Matches 244: Conservative 0: Mismatches 34: Indels 3: Gaps 2:
 Db 375 ACCAGTCTCCAGGACCCCTGCTTTGTCGAGGGGAAAGACACCTCTCTCTGAGG 434
 QY 7 ACACATCTCTATCTATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 66
 Db 435 GCAGTCACAGCTTTAGCAGCAGCTACCTAGCTGCTGCTGCTGCTGCTGCTGCTG 494
 QY 67 GCAGTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 123
 Db 495 CCAGGCTCTCTATCTATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 554
 QY 124 CCAGGCTCTCTATCTATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 183
 Db 555 GCAGTGGTCTGGGACAGACTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCT 614
 QY 184 GCAGTGGTCTGGGACAGACTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCT 243
 Db 615 GCAGTCTATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 655
 QY 244 GCAGTTTATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 284

RESULT 4
 ID PCT-US93-12501-1 STANDARD: DNA: UNC: 325 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 1: Application PC/TUS9312501.
 CC Sequence 1: Application PC/TUS9312501.
 CC GENERAL INFORMATION:
 CC APPLICANT: Chang, Tse Wen
 CC TITLE OF INVENTION: ALLERGEN-SPECIFIC IgA MONOCLONAL ANTIBODIES AND
 CC TITLE OF INVENTION: RELATED PRODUCTS FOR ALLERGY TREATMENT
 CC NUMBER OF SEQUENCES: 10
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Tanox Biosystems, Inc.
 CC STREET: 10301 Stella Link Rd.
 CC CITY: Houston
 CC STATE: Texas

CC COUNTRY: USA
 CC ZIP: 77025
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: 3.5" Hi Density Diskette
 CC COMPUTER: IBM PS/2
 CC OPERATING SYSTEM: Windows, Version 4.0
 CC SOFTWARE: Wordperfect 5.1
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/12501
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER:
 CC FILING DATE:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Mirabel, Eric P.
 CC REGISTRATION NUMBER: 31,211
 CC REFERENCE/DOCKET NUMBER: TNX92-3
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 713-664-2388
 CC TELEFAX: 713-664-8914
 CC INFORMATION FOR SEQ ID NO: 1:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 325 nucleotides
 CC TYPE: nucleic acid
 CC STRANDEDNESS: double stranded
 CC TOPOLOGY: Linear
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: Join(116..163, 351..650)
 CC Sequence 325 bp: 79 A: 93 C: 79 G: 74 T: 0 other:

Query Match 59.0% Score 186: DB 11: Length 325:
 Best Local Similarity 82.3% Prod No 2,22e-118:
 Matches 256: Conservative 0: Mismatches 52: Indels 3: Gaps 2:
 Db 13 AGCAGCTCTCCAGGACCCCTGCTTTGTCGAGGGGAAAGACACCTCTCTCTGAGG 72
 QY 7 AGCAGCTCTCCAGGACCCCTGCTTTGTCGAGGGGAAAGACACCTCTCTCTGAGG 66
 Db 73 GCACATCAGACTTTAGCAGCAGCTACCTAGCTGCTGCTGCTGCTGCTGCTGCTG 132
 QY 67 GCACATCAGACTTTAGCAGCAGCTACCTAGCTGCTGCTGCTGCTGCTGCTGCTG 123
 Db 133 CCAGGCTCTCTATCTATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 192
 QY 124 CCAGGCTCTCTATCTATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 183
 Db 193 GCAGTGGTCTGGGACAGACTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAG 252
 QY 184 GCAGTGGTCTGGGACAGACTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAG 243
 Db 253 GCAGTGTATTATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 312
 QY 244 GCAGTTTATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 303
 Db 313 GTTGAATCAA 323
 QY 304 GTTGAATCAA 314

RESULT 5
 ID PCT-US94-01258-2 STANDARD: DNA: UNC: 645 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 2: Application PC/TUS9401258.
 CC Sequence 2: Application PC/TUS9401258.
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
 CC TITLE OF INVENTION: USING UNIVERSAL OP PANDEMIC IMMUNOGLOBULIN LIGHT
 CC CHAINS
 CC NUMBER OF SEQUENCES: 61
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible

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CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01258
CC FILING DATE: 02-FEB-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 646 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T; 0 other;

Query Match 58.7%; Score 185; DB 12; Length 646;
Best Local Similarity 85.5%; Pred. No. 1.26e-117;
Matches 241; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

Db 1 GAGCTCAGCAGTCTCCAGGACACCTGCTGTTGTTCTCCAGGGGAAAGAGGACACCTCTCC 60
QY 1 GAGCTCAGCAGTCTCCAGGACACCTGCTGTTGTTCTCCAGGGGAAAGAGGACACCTCTCC 60
Db 61 TGCAGGGGTCAGTCAAGTCTTACAGAGGCTTACTAGGCTGTGTAACACAAACCTGAG 120
QY 61 TGCAGGGGTCAGTCAAGTCTTACAGAGGCTTACTAGGCTGTGTAACACAAACCTGAG 117
Db 121 CAGGCTCCAGGCTCCTCATCTATGATATGATACACAGAGGCTGCTGCTATCCAGAGG 180
QY 118 CAGGCTCCAGGCTCCTCATCTATGATATGATACACAGAGGCTGCTGCTATCCAGAGG 177
Db 181 TCCAGTGGCAGTGGGCTGCGGACACATCTCACTCTCACCACATCAGCAGACCTGGAG 240
QY 178 TCCAGTGGCAGTGGGCTGCGGACACATCTCACTCTCACCACATCAGCAGACCTGGAG 237
Db 241 GATTTCGACAGTCTACTGCTCAGCAGATGCTGGCTCAGCG 282
QY 238 GACTTTCGACAGTCTACTGCTCAGCAGATGCTGGCTCAGCG 279

RESULT 6
ID PCT-US94-11235-2 STANDARD; DNA: UNC; 646 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 2, Application PCT/US95/11235
CC Sequence 2, Application PCT/US95/11235
CC GENERAL INFORMATION:
CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10466 North Torrey Pines Road, Torrey
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11235
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CC FILING DATE: 01-SEP-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/300,386
CC FILING DATE: 02-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/826,623
CC FILING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: TSP1 400.1 (PC)
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 646 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T; 0 other;

Query Match 58.7%; Score 185; DB 13; Length 646;
Best Local Similarity 85.5%; Pred. No. 1.26e-117;
Matches 241; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

Db 1 GAGCTCAGCAGTCTCCAGGACACCTGCTGTTGTTCTCCAGGGGAAAGAGGACACCTCTCC 60
QY 1 GAGCTCAGCAGTCTCCAGGACACCTGCTGTTGTTCTCCAGGGGAAAGAGGACACCTCTCC 60
Db 61 TGCAGGGGTCAGTCAAGTCTTACAGAGGCTTACTAGGCTGTGTAACACAAACCTGAG 120
QY 61 TGCAGGGGTCAGTCAAGTCTTACAGAGGCTTACTAGGCTGTGTAACACAAACCTGAG 117
Db 121 CAGGCTCCAGGCTCCTCATCTATGATATGATACACAGAGGCTGCTGCTATCCAGAGG 180
QY 118 CAGGCTCCAGGCTCCTCATCTATGATATGATACACAGAGGCTGCTGCTATCCAGAGG 177
Db 181 TCCAGTGGCAGTGGGCTGCGGACACATCTCACTCTCACCACATCAGCAGACCTGGAG 240
QY 178 TCCAGTGGCAGTGGGCTGCGGACACATCTCACTCTCACCACATCAGCAGACCTGGAG 237
Db 241 GATTTCGACAGTCTACTGCTCAGCAGATGCTGGCTCAGCG 282
QY 238 GACTTTCGACAGTCTACTGCTCAGCAGATGCTGGCTCAGCG 279

RESULT 7
ID US-08-300-386A-2 STANDARD; DNA: UNC; 646 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 2, Application US/08300386A.
CC Sequence 2, Application US/08300386A
CC Patent No. 5667988
CC GENERAL INFORMATION:
CC APPLICANT: Barbas, Carlos F. III
CC APPLICANT: Burton, Dennis P.
CC APPLICANT: Lerner, Richard A.
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT
```



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CHAINS
CC  NUMBER OF SEQUENCES: 70
CC  CORRESPONDENCE ADDRESS:
CC  ADDRESSEE: The Scripps Research Institute
CC  STREET: 10566 No 56798th Torrey Pines Road, LPe8
CC  CITY: La Jolla
CC  STATE: CA
CC  COUNTRY: USA
CC  ZIP: 92037
CC  COMPUTER READABLE FORM:
CC  MEDIUM TYPE: Floppy disk
CC  COMPUTER: IBM PC compatible
CC  OPERATING SYSTEM: PC-DOS/MS-DOS
CC  SOFTWARE: PatentIn Release #1.0, Version #1.25
CC  CURRENT APPLICATION DATA:
CC  APPLICATION NUMBER: US/08/300,386A
CC  FILING DATE: 02-SEP-1994
CC  CLASSIFICATION: 435
CC  PRIOR APPLICATION DATA:
CC  APPLICATION NUMBER: US 08/174,674
CC  FILING DATE: 28-DEC-1993
CC  PRIOR APPLICATION DATA:
CC  APPLICATION NUMBER: US 07/826,523
CC  FILING DATE: 27-JAN-1992
CC  PRIOR APPLICATION DATA:
CC  APPLICATION NUMBER: US 07/454,148
CC  FILING DATE: 30-SEP-1992
CC  PRIOR APPLICATION DATA:
CC  APPLICATION NUMBER: US 08/012,555
CC  FILING DATE: 02-FEB-1994
CC  ATTORNEY/AGENT INFORMATION:
CC  NAME: Fitting, Thomas
CC  REGISTRATION NUMBER: 34,163
CC  REFERENCE/DOCKET NUMBER: TSP1 409.1
CC  TELECOMMUNICATION INFORMATION:
CC  TELEPHONE: 619-554-2937
CC  TELEFAX: 619-554-6312
CC  INFORMATION FOR SEQ ID NO: 2:
CC  SEQUENCE CHARACTERISTICS:
CC  LENGTH: 645 base pairs
CC  TYPE: nucleic acid
CC  STRANDEDNESS: single
CC  TOPOLOGY: linear
CC  MOLECULE TYPE: cDNA
CC  HYPOTHETICAL: NO
CC  ANTI-SENSE: NO
CC  Sequence 646 BP: 162 A: 187 C: 170 G: 127 T: 0 other:

Query Match      58.7%; Score 185; DB 7; Length 645;
Best Local Similarity 85.5%; Pred. No. 1.26e-117;
Matches 241; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

Db  1  GAGCTCAGCGAGTCTCCAGGCACTGCTTTGTCTCCAGGGGAAAGAGGACCCCTCTCC 60
QY  1  GAGCTCAGCGAGTCTCCAGGCACTGCTTTGTCTCCAGGGGAAAGAGGACCCCTCTCC 60

Db  61  TCAGGCGCAGTACAGAGTGTATACAGGAGGAGTGTATAGTGTATAGTGTATAGTGTATAG 120
QY  61  TCAGGCGCAGTACAGAGTGTATACAGGAGGAGTGTATAGTGTATAGTGTATAGTGTATAG 117

Db  121  CAGGCTCCAGGAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAG 180
QY  118  CAGGCTCCAGGAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAG 177

Db  181  TCAGTGTAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAG 240
QY  178  TCAGTGTAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAG 237

Db  241  GATTTTGCAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAG 282
QY  238  GACTTTTGCAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAGTGTATAG 279

RESULT 8
ID  US-08-276-852-152 STANDARD: DNA; UNC: 729 BP.
AC  xxxxxx
DT  01-JAN-1900
UE  Sequence 152, Application US/08276852.
CC  Sequence 152, Application US/08276852
CC  Patent No. 5652138
CC  GENERAL INFORMATION:
CC  APPLICANT: Burton, Dennis R
CC  APPLICANT: Barbas, Carlos F
CC  APPLICANT: Lerner, Richard A
CC  TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC  TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC  NUMBER OF SEQUENCES: 170
CC  CORRESPONDENCE ADDRESS:
CC  ADDRESSEE: The Scripps Research Institute, Office of
CC  ADDRESSEE: Patent Counsel
CC  STREET: 10666 No 5652138th Torrey Pines Road, Suite 220.
CC  STREET: Mail Drop TPC8
CC  CITY: La Jolla
CC  STATE: CA
CC  COUNTRY: USA
CC  ZIP: 92037
CC  COMPUTER READABLE FORM:
CC  MEDIUM TYPE: Floppy disk
CC  COMPUTER: IBM PC compatible
CC  OPERATING SYSTEM: PC-DOS/MS-DOS
CC  SOFTWARE: PatentIn Release #1.0, Version #1.25
CC  CURRENT APPLICATION DATA:
CC  APPLICATION NUMBER: US/08/276,852
CC  FILING DATE: 18-JUL-1994
CC  CLASSIFICATION: 514
CC  PRIOR APPLICATION DATA:
CC  APPLICATION NUMBER: US 08/178,302
CC  FILING DATE: 30-SEP-1993
CC  PRIOR APPLICATION DATA:
CC  APPLICATION NUMBER: US 07/954,148
CC  FILING DATE: 30-SEP-1992
CC  ATTORNEY/AGENT INFORMATION:
CC  NAME: Fitting, Thomas
CC  REGISTRATION NUMBER: 34,163
CC  REFERENCE/DOCKET NUMBER: SCRI452P
CC  TELECOMMUNICATION INFORMATION:
CC  TELEPHONE: 619-554-2937
CC  TELEFAX: 619-554-6312
CC  INFORMATION FOR SEQ ID NO: 152:
CC  SEQUENCE CHARACTERISTICS:
CC  LENGTH: 729 base pairs
CC  TYPE: nucleic acid
CC  STRANDEDNESS: double
CC  TOPOLOGY: linear
CC  MOLECULE TYPE: DNA (genomic)
CC  FEATURE:
CC  NAME/KEY: CDS
CC  LOCATION: 9..715
CC  Sequence 729 BP: 173 A: 208 C: 192 G: 156 T: 0 other:

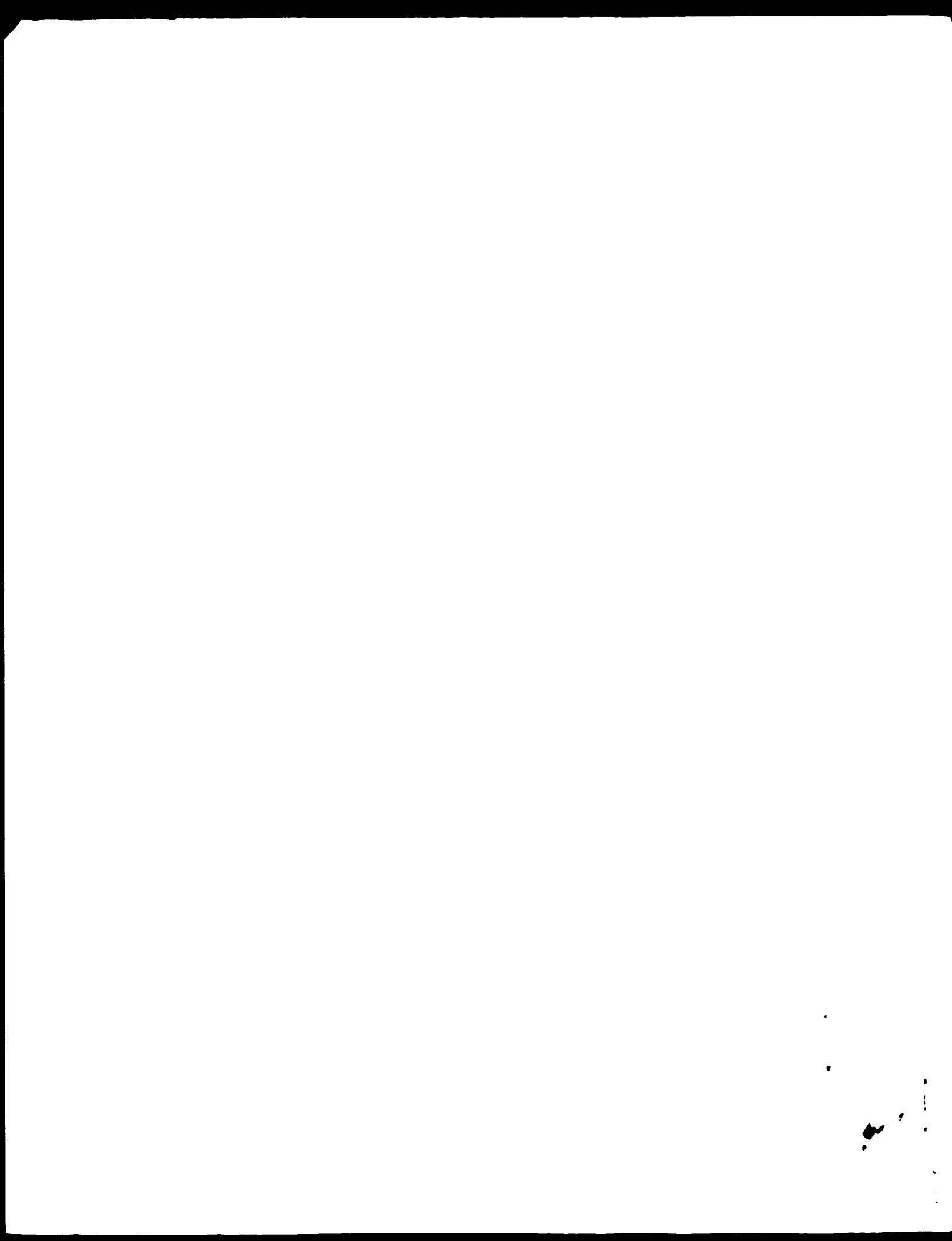
Query Match      51.4%; Score 162; DB 7; Length 729;
Best Local Similarity 78.6%; Pred. No. 2.41e-100;
Matches 243; Conservative 0; Mismatches 53; Indels 3; Gaps 2;

Db  78  CTCAGCGAGTCTCCAGGCACTGCTTTGTCTCCAGGGGAAAGAGGACCCCTCTCTGT 197
QY  4  CTCAGGAGTCTCCAGGCACTGCTTTGTCTCCAGGGGAAAGAGGACCCCTCTCTGT 64

Db  138  AGGTCAGTCTCAGCAGTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197
QY  64  AGGTCAGTCTCAGCAGTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

Db  198  GTTCAGGAGTCTCAGCAGTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 257
QY  121  GTTCAGGAGTCTCAGCAGTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
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Search completed: Tue Feb 24 14:19:44 1998
Job time : 55 secs.



Matches 241; Conserv

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Query Match      64.98;   Score 204;   DB 12;   Length 812;
Rest Loca: Similarity 86.78;   Proj N, 27e-119;
Matches 241; Conservative 0; Mismatches 37; Indels

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Journal Pre-proof

KW passive immunity: group B streptococci; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT sig_peptide 1..49
 FT /tag= a
 FT /note= "leader"
 FT misc_RNA 50..388
 FT /tag= b
 FT /label= L'V 1
 FT /note= "encodes last 3 amino acids of leader and the rearranged VJ gene"
 FT misc_RNA 389..726
 FT /tag= c
 FT /label= L'V 2
 FT /note= "encodes last 3 amino acids of leader and the rearranged VJ gene"
 FT misc_RNA 728..1044
 FT /tag= d
 FT /note= "constant region"
 FT polyA_signal 1221..1226
 FT /tag= e
 PN W09106305-A.
 PD 16-MAY-1991.
 PE 06-NOV-1990: U06426.
 PR 07-NOV-1989: US-432700.
 PA (BPIW) RPISTOL-MYERS SQUIR
 PI Shuford WW, Harris LJ, Raff HV;
 DR WPI: 91-163947/22.
 DR P-PSDB: R12128.
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 PS Claim 42: Fig 16: 104pp. English.
 CC This sequence encodes an aberrant light chain containing two L'V
 CC regions. Antibody molecules of the invention can include one or two
 CC such aberrant light chains to produce heavier antibodies. These
 CC heavier antibodies were found to have higher avidity than antibodies
 CC with just a single copy of the L'V region. The clone is not
 CC complete; it starts with the 5' of the AUG initiator codon.
 CC See also Q11879 and Q11880.
 SQ Sequence 1242 BP; 291 A; 383 C, 302 G, 266 T.
 Query Match 63.5%; Score 200; DB 2; Length 1242;
 Best Local Similarity 88.8%; Pred. No 5 19e-116;
 Matches 229; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 Db 71 aaacagctccagccaccctctcttctctccaggggaagagccaccctctctcaggg 130
 QY 7 AGCGACTCTCCAGCCACCCCTGTCTGTCTCTCCAGGGGAAAGAGGCTCCCTCTCCAGG 66
 Db 131 gccagtcagagtggtggcagctacttagcctggfaccacagagaacctggccggctccc 190
 QY 67 GCCAGTCAGAGTGTGGTAACAAATTAGCTTGGTATCAGCAGAAACCTGGCCAGGCTCCC 126
 Db 191 aggcctccatcatgatgcattccacagggccactggcattccacagccaggttcagtgcc 250
 QY 127 AGGCTCTCATTTATGGTGGAAACACAGAGCCACTGGTACCCAGACAGAGTTTCAGTGGC 186
 Db 251 atggggtctggagagacttcaactctcaactcagcagcctagagcctgaagattttgca 310
 QY 187 AGTGGGCTGSSGACAAATTTCACTCTCACTATCAAGCCTGTGAGCTGTGAGGACTTTGCA 246
 Db 311 gttattactgtcaaac 328
 QY 247 GTTTATTCTGTCAACAC 264
 RESULT 11
 ID Q49155 standard; cDNA; 387 BP.
 AC Q49155;
 DT 21-NOV-1993 (first entry)
 DE Fl05-rearranged variable region light chain.
 KW Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;

KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT sig_peptide 1..57
 FT /tag= a
 FT mat_peptide 58..387
 FT /tag= b
 PN W09312232-A.
 PD 24-JUN-1993.
 PE 10-DEC-1992: U10928.
 PR 10-DEC-1991: US-804552.
 PA (DAND) DANA FARBER CANCER INST INC
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 PI Haseltine WA, Marasco WA, Posner MP, Sedroski IG;
 DR WPI: 93-214174/26.
 DR P-PSDB: R41286.
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Claim 1: Page 79: 109pp: English.
 CC mRNA from the known hybridoma F105 was converted to cDNA and this
 CC subjected to PCR amplification using primers corresp. to appropriate
 CC parts of the heavy or light chains and having restriction sites to
 CC permit cloning. The extension prods. were isolated and sequenced.
 CC The recombinant human monoclonal antibody (MAb) binds to a
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad
 CC range of HIV isolates. The MAb may be used to treat immune
 CC deficiency, esp. at doses of 0.1-10 mg/kg.
 SQ Sequence 387 BP; 88 A; 111 C; 101 G; 87 T;
 Query Match 62.2%; Score 196; DB 7; Length 387;
 Best Local Similarity 83.4%; Pred. No 2.89e-113;
 Matches 261; Conservative 0; Mismatches 47; Indels 3; Gaps 2;
 Db 73 acgcagctccagcaccctctcttctgtcaggggaagagccaccctctctcaggg 132
 QY 7 AGCAGCTCTCCAGCCACCCCTGTCTGTCTCTCCAGGGGAAAGAGGCTCCCTCTCCAGG 66
 Db 133 gccagtcagagtggttagcagcaggtacttagcctggtaccagcaaacctggccagct 192
 QY 67 GCCAGTCAGAGTGTGGTAACAA-T-TT-AGCTTGTGTATCAGCAGAAACCTCCAGGCT 123
 Db 193 gccagtcctctctctctctctctctcagcagcagcagcagcagcagcagcagcagc 252
 QY 124 CCCAGGCTCTCTCATTTAAGGTTGGAACACACAGAGACCTGGTACACAGGTTCACT 183
 Db 253 ggcagtggtgctgggacagagcttcaactctcaccatcagcagagtgagcctaaagatttt 312
 QY 184 GGCAGCTGGGCTGGGACAGAGATTTCACCTTCACATATCAGTACAGTACAGTACAGT 243
 Db 313 gcagtgattactgtcagcaaatatgataactcagttgtactcttggccagggagcagga 372
 QY 244 GCAGTTATTCTGTCAACACTATAGTACCTGCGGCTCCTCTTGGCGGGGAGCCCAAG 303
 Db 373 ctggagatcaa 383
 QY 304 GTCAGTTCAA 314
 RESULT 12
 ID Q42707 standard; DNA; 390 BP.
 AC Q42707;
 DT 01-NOV-1993 (first entry)
 DE Fl05VK-F105Jk.
 KW Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT sig_peptide 1..60
 FT /tag= a

```

FT mat_protein 61...390
FT /*tag= b 1 351
FT misc_RNA 1
FT /*tag= c 352...390
FT label= F105VK
FT misc_RNA 352...390
FT /*tag= d
FT label= F105Jk
FT misc_RNA 130...165
FT /*tag= e
FT label= CDR1
FT misc_RNA 211...231
FT /*tag= f
FT label= CDR2
FT misc_RNA 328...354
FT /*tag= g
FT label= CDR3
PN W09312232-A.
PD 24-JUN-1993
PR 10-DEC-1992: US-804652
PR 10-DEC-1992: U10928.
PA (DAND ) DNA FABER CANCER INST INC.
PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
DR WPI; 93-214174/26
DR P-PSDB; R38672.
PT DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV, for treating AIDS, and for diagnosing and
PT monitoring HIV infection
PS Disclosure: Page 73-74; 109pp; English.
CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from
CC other F105 VK sequences given elsewhere in the specification) was
CC compared with germline gene Humv4325 (342706), showing 87.7%
CC similarity. By nucleotide sequence analysis, F105 appears to
CC be derived from a member of the VH III subgroup gene family.
SQ Sequence 390 BP; 91 A; 115 C; 102 G; 97 T.

Query Match 61.0%; Score 192; DB 7; Length 390.
Best Local Similarity 85.4%; Pred No. 1-60e-110;
Matches 268; Conservative 0; Mismatches 40; Indels 6; Gaps 4.

Db 73 accagcttcaggacacccctctgttctccagggaagaaagcaccctctctcagg 112
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 7 ACCGAGCTTCAGACACACCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 113
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 133 gcaatcgaagatattacagagagagagagagagagagagagagagagagag 192
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 GCAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 193
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 193 ccagagcttcctatctatctatctatctatctatctatctatctatctatct 252
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 124 CCAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 183
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 253 gcaatcgaagatattacagagagagagagagagagagagagagagagagag 312
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 184 GCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 313 gcaatcgaagatattacagagagagagagagagagagagagagagagagag 372
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 244 GAGATTTATTTTGTCAACACTATAGATCTCTCTCTCTCTCTCTCTCTCT 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 gcaatcgaagatattacagagagagagagagagagagagagagagagagag 390
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 AAGCTCGAGATTCAA 314
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
ID Q44224 standard: DNA; 900 BP.
AC Q44224:
DT 10-NOV-1993 (first entry)
DE Human DNA fragment vk65.8 containing V-kappa gene segment.
KW Immunoglobulin: light chain variable region; minilocus;
KW isotype switching; rearranged functional VH gene segment;

```

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KW human light chain transgene; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_signal 53...60
FT /*tag= a
FT /note= "splicing and recombination signal ?"
FT exon 116...164
FT /*tag= b
FT /number= 1
FT /note= "nucleotides 116-118 represent the
FT initiation codon, i.e. the start of the ORF;
FT the precise start point of the exon is not
FT indicated"
FT intron 165...351
FT /*tag= c
FT exon 352...650
FT /*tag= d
FT /note= "ORF not terminated by a stop codon"
FT misc_recomb 653...680
FT /*tag= e
FT /note= "splicing and recombination signal sequence"
PN W09312227-A.
PD 24-JUN-1993
PR 17-DEC-1992: U10983.
PR 17-DEC-1992: US-810279.
PR 18-MAR-1992: US-853408.
PR 23-JUN-1992: US-904068.
PA (GENP-) GENPHARM INT INC.
PI Kay RM, Lonberg N;
DR WPI; 93-214169/26.
DR P-PSDB; R38650.
PT Transgenic non-human animals contg. immunoglobulin heavy chain
PT trans. 3662 - used to produce useful antibodies by isotype
PT switching.
PS Example 21; Fig 43; 196pp; English.
CC The V-kappa specific oligonucleotide 69027 was used to probe a
CC human placental genomic DNA library cloned into lambdaEMBL3/SPL677.
CC DNA fragments containing V-kappa segments from positive phase
CC clones were subcloned into plasmid vectors. Variable gene segments
CC from the resulting clones were sequenced and functional clones were
CC selected on the basis of open reading frames, intact donor and
CC acceptor splice sites and intact recombination sequences. The
CC sequences obtained from four different plasmid clones were
CC designated: pVK 3, pVK 5, pVK 6 and pVK 7 (see 341-25).
CC respectively.
SQ Sequence 560 BP; 200 A; 241 C; 201 G; 238 T.

Query Match 61.0%; Score 192; DB 7; Length 900.
Best Local Similarity 86.8%; Pred No. 1-60e-110;
Matches 244; Conservative 0; Mismatches 34; Indels 4; Gaps 4.

Db 375 accgagcttcaggacacccctctgttctccagggaagaaagcaccctctctcagg 434
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 7 ACCGAGCTTCAGACACACCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 435
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 435 gcaatcgaagatattacagagagagagagagagagagagagagagagagag 494
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 GCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 554
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 495 ccagagcttcctatctatctatctatctatctatctatctatctatctatct 614
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 124 CCAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 683
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 614 gcaatcgaagatattacagagagagagagagagagagagagagagagagag 655
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 184 GCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 724
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 gcaatcgaagatattacagagagagagagagagagagagagagagagagag 784
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 244 GCAGTTTATTTTGTCAACACTATAGATCTCTCTCTCTCTCTCTCTCTCT 884
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14

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ID Q78854 standard; DNA: 900 BP.
 AC Q78854;
 DE 07-JUN-1995 (first entry)
 DT Human V-kappa gene vk65.8.
 KW Transgenic mouse; transgenic animal; antibody engineering;
 KW variable region; light chain; minilocus transgene;
 KW chimeric antibody; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 116..650
 FT /*tag= a
 FT intron b 163..350
 FT /*tag= b
 FT misc_signal 553..659
 FT /*tag= c
 FT /*tag= Splicing_signal
 FT misc_signal 672..680
 FT /*tag= d
 FT /*label= Recombination_signal
 PN W09425585-A.
 PD 10-NOV-1994.
 PE 25-APR-1994; U04580.
 PR 26-APR-1993; US-053131.
 PR 22-JUL-1993; US-066762.
 PR 18-NOV-1993; US-155301.
 PR 03-DEC-1993; US-161739.
 PR 10-DEC-1993; US-165699.
 PR 09-MAR-1994; US-209741.
 PA (GENP-) GENPHARM INT INC.
 PI Kay RM, Lonberg N;
 DR WPI: 94-358263/44.
 DR P-PSDB: P62930.
 PT Transgenic non-human animals producing heterologous or chimeric
 PT antibodies - for binding a pre-determined human antigen with
 PT increased affinity
 PS Disclosure, Fig. 43, 295pp, English.
 CC Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in
 CC Q78852-Q78855, respectively) each contain a V-kappa gene segment
 CC that can be used to form a complete human light chain minilocus
 CC transgene for expression in a nonhuman transgenic animal for
 CC heterologous antibody production. The deduced amino acid
 CC sequences of the V-kappa coding regions are given in P62928-P62931
 SQ Sequence 900 BP; 220 A; 241 C; 201 G; 238 T;

 Query Match 61.0%; Score 192; DB 12; Length 900;
 Best Local Similarity 86.8%; Pred No 1 60e-110;
 Matches 244, Conservative 0, Mismatches 34, Indels 3, Gaps 2.

 Db 375 acgcagctccagcagccctgtctgtctccaggggaagagccacccctctctcagc 434
 QY 7 ACGCAGCTCCAGCAGCCCTGTCTGTCTCCAGGGGAAAGAGCCTCTCTCTGCGAGG 66

 Db 435 gccagtcagagtgtagcagcagctacttagcctgtgtaccagcagagaacccctgccagct 494
 QY 67 GCCAGTCAGAGTGTCGGTAACAA-T--TTAGCTTGTGTATCAGCAGAAACCTGGCCAGGCT 123

 Db 495 cccagctccctcatctatgtgtccagcagggccactggtccatccacagagttcagt 554
 QY 124 CCCAGCTCCTCATTTATGGTGGAAACACAGAGCTACTGGTACCCACAGAGTTCACT 183

 Db 555 gccagtggtgtggacagactctcctccatccagcagactggagcctgaagatttt 614
 QY 184 GGCAGTGGGTCTGGACAGAAATTCATCTCTCACTCCTCACTAGCTGTGAGGACTTT 243

 Db 615 gccagtgattactgcacagtagtagtagcctccctccac 655
 QY 244 GCAGTTATTCTGTCAACACTATAGTACCTGGCCGCTCAC 284

 Search completed: Tue Feb 24 09:20:24 1998
 Job time : 88 secs.

DE DNA fragment vk65.8, containing variable kappa chain gene.
 KW Variable; kappa chain; gene segment; human; DNA fragment; vk65.8;
 KW unrearranged; light chain; minilocus; transgene; transgenic; mouse;
 OS production; heterologous; antibody; gamma, immunoglobulin; ss.
 FH Homo sapiens.
 Key Location/Qualifiers
 FT exon 116..164
 FT /*tag= a
 FT exon 352..650
 FT /*tag= b
 PN US5545806-A.
 PD 13-AUG-1996. 574748.
 PE 29-AUG-1990; US-574748.
 PR 29-AUG-1990; US-575962.
 PR 31-AUG-1991; US-810279.
 PR 17-DEC-1991; US-853408.
 PR 18-MAR-1992; US-904068.
 PR 23-JUN-1992; US-990860.
 PR 16-DEC-1992; US-990860.
 PA (GENP-) GENPHARM INT INC.
 PI Kay RM, Lonberg N;
 DR WPI: 96-383736/38.
 DR P-PSDB: W03948.
 PT Prodn. of heterologous human immunoglobulin(s) - by immunising
 PT transgenic mice
 PS Example 21; Fig 43; 94pp; English.
 CC The present sequence is the variable kappa chain gene segment
 CC containing human DNA fragment, vk65.8, which was co-injected along
 CC with the human DNA fragments vk65.3, vk65.5 and vk65.15 into half
 CC day mouse embryo pronuclei, to generate an unrearranged light chain
 CC minilocus transgene. The resulting transgenic mice can be used for
 CC the production of heterologous (i.e. human) antibodies against
 CC specific antigens, this comprises immunising a mouse with a
 CC preselected antigen and collecting antigen binding heterologous
 CC human gamma immunoglobulins.
 SQ Sequence 900 BP; 220 A; 241 C; 201 G; 238 T;

 Query Match 61.0%; Score 192; DB 47; Length 900;
 Best Local Similarity 86.8%; Pred No 1 60e-110;
 Matches 244, Conservative 0, Mismatches 34, Indels 3, Gaps 2.

 Db 375 acgcagctccagcagccctgtctgtctccaggggaagagccacccctctctcagc 434
 QY 7 ACGCAGCTCCAGCAGCCCTGTCTGTCTCCAGGGGAAAGAGCCTCTCTCTGCGAGG 66

 Db 435 gccagtcagagtgtagcagcagctacttagcctgtgtaccagcagagaacccctgccagct 494
 QY 67 GCCAGTCAGAGTGTCGGTAACAA-T--TTAGCTTGTGTATCAGCAGAAACCTGGCCAGGCT 123

 Db 495 cccagctccctcatctatgtgtccagcagggccactggtccatccacagagttcagt 554
 QY 124 CCCAGCTCCTCATTTATGGTGGAAACACAGAGCTACTGGTACCCACAGAGTTCACT 183

 Db 555 gccagtggtgtggacagactctcctccatccagcagactggagcctgaagatttt 614
 QY 184 GGCAGTGGGTCTGGACAGAAATTCATCTCTCACTCCTCACTAGCTGTGAGGACTTT 243

 Db 615 gccagtgattactgcacagtagtagtagcctccctccac 655
 QY 244 GCAGTTATTCTGTCAACACTATAGTACCTGGCCGCTCAC 284

 Search completed: Tue Feb 24 09:20:24 1998
 Job time : 88 secs.

RESULT 15
 ID 17182 standard; DNA: 900 BP.
 AC T37442;
 DT 14-APR-1997 (first entry)


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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 413.
Location/Qualifiers
1..418
/organism="Homo sapiens"
/note="Vector: pAMP10; mRNA made from liposarcoma. cDNA
made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Preference: Krizman et al. (1996) Cancer Research
56:5380-5383."
/cclone="940044"
/cclone_lib="NCI_CGAP_lip2"
/tissue_type="liposarcoma"

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mrna      99 a 127 c 102 g 90 t
<1...>418
BASE COUNT
ORIGIN

Query Match 74 59: Score 237; DP 39; Length 418;
Best Local Similarity 88 88; Prod. No. 0 000-00;
Matches 277; Conservative 0; Mismatches 34; Indels 1; Gaps 1:

Db 95 acgcagctccaggcacctctttgtctccaggggaaaggacccctctcttgagg 154
|||||
QY 7 AGCGACTGTCAGGACCTGTCTCTTGTCTCCAGGGGAAGAGACACCTCTCTGAG 66
|||||

Db 155 gccagtcagagtatcatcagcacccccctttagctggtatcagcaaaaacctggccagact 214
|||||
QY 67 GGCAGTCCAGAGTGTAGAGAACTACTTAGCTGGTATGATCAGAAAAACTTGGCAGGCT 126
|||||

Db 215 ccaggctctctcatctcaggtgcatacagacggccactgg-atccagacagagttcaat 273
|||||
QY 127 CCGCAGGCTCCATCTATGTGTTATCCAGCAGGAGGCCACTGGCATCCACACAGGTTCAAT 186
|||||

Db 274 ggcatttgcctgaggacagacttcagctccactcgcagactcgagacctgaaattct 333
|||||
QY 187 GGCAGTGGGTTGGGGATAGACTTCACTCTTCACTATAGTAGAGCTGGAGGCTTGAAGAAT 246
|||||

Db 334 gcagttactattgtcagcacactatggtacatctcatatgagacattcggccagggagcag 393
|||||
QY 247 GCAGTGTATATCTGTACAGCAATGGTAGCTCAATCTGATATTTCTGGTACAGGAGCAAG 406
|||||

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DB 394 gggaattccaa 405
   ||| |||||
QY 307 TTGGAGATCAA 318

RESULT 3
ID HS130877 standard; RNA; EST; 418 BP.
AC AA515239;
NI Q234839
DT 15-JUL-1997 (Rel. 52, Created)
DT 24-JUL-1997 (Rel. 52, Last updated, Version 2)
DE ng6c-07 s1 NCI-CGAP Lip2 Homo sapiens cDNA clone 540044 similar to
DE db_M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN)).
KW EST.
OS Homo sapiens (human)
OC Eukaryota; Eukaryotes, Metazoa; Chordata,
OC Vertebrata; Mammalia, Eutheria, Primates, Catarrhini, Hominidae;
OC Homo.
RN [1]
RP 1-418
RA NCI-CGAP;
FT "National Cancer Institute, Center for Genome Anatomy Project (CGAP).

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RT Tumor Gene Index:
RL Unpublished
CC Contact: Robert Strausberg Ph.D. Tel: (301) 496-1560 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: L. Jeffrey Medeiros,
CC M.D., Michael P. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation:
CC David R. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
CC DNA Sequencing by: Washington University Genome Sequencing Center
CC Clone Distribution: NCI-CGAP clone distribution information can be
CC found through the I M A G E Consortium/LLNL at:
CC www.biol.nsl.gov/ibrrp/image/image.htm Insert Length: 1070 Std
CC Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality
CC sequence stop: 413.
PH Key
PH Location/Qualifiers
FT source
FT 1..418
FT /organism="Homo sapiens"
FT /note="vector: pAMP10; mRNA made from liposarcoma, cDNA
FT made by oligo-dT priming. Non-directionally cloned.
FT Size-selected on agarose gel, average insert size 600 bp
FT Reference: Krizman et al (1996) Cancer Research
FT 56:5380-5383."
FT /clone="940044"
FT /clone_lib="NCI-CGAP_Lip2"
FT /tissue_type="liposarcoma"
FT /lab_host="DH10B"
FT mRNA
FT <1..>418
FT Sequence 418 bp: 99 A; 127 C; 102 G; 90 T; 0 other:

Query Match 74.5% Score 237; DB 71; Length 418;
Best Local Similarity 98.8% Pred. No. 0.00e+00;
Matches 277; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

Db 95 agcagcttcacagcaccctctcttctctcaggggaagagccaccctctcttcagg 154
QY 7 AGCGAGGCTCAGGACGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 66

Db 155 gccatcagaatcatcatcagcaccctctcctcctggtatcagcaaaaacctggccaggt 214
QY 67 GCACATCAGAGTGTATGAGAGAAACATCTTATCTTGGTACACAGCAAAACCTT 126

Db 215 ttttgggtctctctctctctctctctctctctctctctctctctctctctctct 273
QY 127 GCACAGGCTCAGGACGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 186

Db 274 gaaatctctctctctctctctctctctctctctctctctctctctctctct 333
QY 197 GCACATCAGAGTGTATGAGAGAAACATCTTATCTTGGTACACAGCAAAACCTT 245

Db 334 gcaatctctctctctctctctctctctctctctctctctctctctctctct 393
QY 247 GCAGTGTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 306

Db 394 atcgaatacaaa 405
QY 307 TTGGAGATCAAA 318

RESULT 4
ID HS1269512 standard; RNA; EST: 242 BP.
AC AA479857
NI 92205743
DI 23-JUN-1997 (rel 52, Created)
DE 23-JUN-1997 (rel 52, Last updated, Version 1)
DE z35b05.r1 Soares ovary tumor N8HOT Homo sapiens cDNA clone 739953
DE 5' similar to gb:X06764 IG KAPPA CHAIN PRECURSOR V-III REGION
DE (HUMAN):
KW EST.
OS Homo sapiens (human)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea;
RN [1]
RP 1-242
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
Krizman D., Kuraba T., Lacy M., Lennon G., Maizumi M.,

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RA Krizman D., Kuraba T., Lacy M., Lennon G., Maizumi M.,
RA Martin J., Moore B., Schellenberg K., Steptoe M., Tan P.,
RA Thaising H., Whire Y., Wylie T., Waterston P., Wilson R.,
RA "WashU-NCI human EST Project";
RL Unpublished.
CC Contact: Wilson PK Washington University School of Medicine 4444
CC Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 266
CC 1800 Fax: 314 266 Email: est@wustl.edu This clone is
CC available royalty-free through LLNL; contact the IMAGE Consortium
CC (infoimage@llnl.gov) for further information. Seq primer: -28ml3
CC rev2 ET from Amersham.
PH Key
PH Location/Qualifiers
FT source
FT 1..242
FT /organism="Homo sapiens"
FT /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
FT modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
FT strand cDNA was primed with a Not 1 - oligo(dT) primer [5'
FT TGTTACCAATCTCAAGTGGAGGCGGCGGGGTTTTTTTTTTTTTTT 3'].
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not 1 and cloned into
FT the Not 1 and Eco RI sites of a modified pT7T3 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M. Fatima Bonaldo."
FT /clone="739953"
FT /clone_lib="Soares ovary tumor N8HOT"
FT /sex="Female"
FT /tissue_type="ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
FT mRNA
FT <1..>242
FT Sequence 242 bp: 54 A; 56 C; 59 G; 53 T; 0 other:

Query Match 66.4% Score 211; DB 64; Length 242;
Best Local Similarity 94.6% Pred. No. 0.00e+00;
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QY 71 GTCAAGGTGTAGGAGCAACTACTTACCTTGGTACCAAGTAAAGATTTGGTATG 130

Db 61 agcctctctctctctctctctctctctctctctctctctctctctctctctct 120
QY 131 GGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 190

Db 121 gtcctctctctctctctctctctctctctctctctctctctctctctctct 180
QY 191 GTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249

Db 181 gtttattctctctctctctctctctctctctctctctctctctctctctct 240
QY 250 GTGTATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 309

Db 241 ga 242
QY 310 GA 311

RESULT 5
LOCUS AA479857 242 bp TERA EST 12-JUN-1997
DEFINITION z35b05.r1 Soares ovary tumor N8HOT Homo sapiens cDNA clone 739953
DEFINITION 5' similar to gb:X06764 IG KAPPA CHAIN PRECURSOR V-III REGION
ACCESSION AA479857
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
REFERENCE 1 (bases 1 to 242)
AUTHORS Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
Krizman D., Kuraba T., Lacy M., Lennon G., Maizumi M.,

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Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28ml3 rev2 ET from Amersham.
 Location/Qualifiers
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 TGTTACCAATCTGAAGTGGAGGCGCGGTTTITTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
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 (Pharmacia). Library constructed by Bento Soares and
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 QY 131 ggctctctatctatggtggtatctagcagggcgacactggtggtatctccagcaggtt 190
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 Db 181 gttattactgtcagcagctatgtagctcaccgtcaccctttcggcgaggagaccaggtg 240
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 AC AA434001:
 NI G2138915
 DT 01-JUN-1997 (Rel. 52, Created)
 DE 01-JUN-1997 (Rel. 52, Last updated, Version 1)
 DE zw23f01.r1 Soares ovary tumor NcHOT Homo sapiens cDNA clone 770705
 DE 5' similar to gb:z11894 IG KAPPA CHAIN PPECPSOP V-III REGION
 DE (HUMAN):
 KW EST.
 OS Homo sapiens (human)
 OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 FN [1]
 RP 1-269
 RA Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
 Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
 Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
 White Y., Wylie T., Waterston R., Wilson R.,
 RT "WashU-Merck EST Project 1997";
 RL Unpublished.
 CC Contact: Wilson RK WashU-Merck EST Project Washington University
 School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
 CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
 CC est@wustl.edu This clone is available royalty-free through
 CC LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for
 CC further information. Seq primer: -28ml3 rev2 ET from Amersham.
 FH Location/Qualifiers
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 TGTTACCAATCTGAAGTGGAGGCGCGGTTTITTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."
 /clone="770329"
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 QY 67 gccagctcagagctgttaccagcagcacttagcctggtaccagcagaaacctggcaggct 126
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 QY 127 cccaggtct 177
 RESULT 7
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 3' similar to gb:X06764 IG KAPPA CHAIN PPECPSOP V-III REGION
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 Homo.
 REFERENCE 1 (bases 1 to 171)
 AUTHORS Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
 Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
 Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,
 Theising B., White Y., Wylie T., Waterston R. and Wilson R.
 WashU-NCI human EST Project
 Unpublished (1997)
 TITLE
 JOURNAL


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FEATURES
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    double-stranded cDNA was size selected, ligated to Eco RI
    adapters (Pharmacia), digested with Not I and cloned into
    the Not I and Eco RI sites of a modified pT7T3 vector
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    M.Fatima Bonaldo."
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    /sex="Female"
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  QY      67 GCCAGTCAGAGGTTTAGCAGCAACTTACTTAGCTTGTACGACGAGCAAAACCTGGCCAGGCT 126

  Db      197 cccaggtctctctatgtgtgcatccaccagggccactggtatccagccaggttcaga 256
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  QY      127 CCCAGGCTCCTCATCTATGGTGTATCCAGCAGGCGCCACTGGCATCCCGACAGAGGTTTCAG- 185

  Db      257 tagcagtggtctagcagaggttcactct 287
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  QY      186 TGGCAGTGGGCT-GGGACAGACTTCACCT 215

  RESULT  10
  ID      HS1258064 standard; RNA; EST; 324 BP.
  AC      AA484224;
  NI      92189108
  DT      13-JUN-1997 (Rel. 52, Last updated, Version 1)
  DE      zx83c06.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone 810346
  DE      5' similar to gb:M12740_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION
  DE      (HUMAN);.
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  OS      Homo sapiens (human)
  OC      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
  OC      Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
  RN      [1]
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  RA      Kuraba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
  RA      Moore B., Schellenberg K., Shapiro M., Tan F., Theising J.,
  RA      White Y., Willie T., Waterston R., Wilson R.
  FT      "Washington EST Project 1997".
  RL      Unpublished
  CC      Contact: Wilson RK WashU-Merck EST Project Washington University
  CC      School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
  CC      MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email
  CC      est@wustl.wustl.edu This clone is available royalty-free through
  CC      LNLN; contact the IMAGE Consortium (info@image.llnl.gov) for
  CC      further information. Seq primer: -28m13 rev2 ET from Amersham High
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mRNA

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Search completed: Tue Feb 24 08:08:45 1998
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Db 133 aggcctctcatctatgtgtcatccaccagggccactggtatccagcagaggttcagtgcc 192
QY 127 AGGCTCTCATTTATGTGTGGAACACACAGAGCCACTGGTACCCAGACAGAGTTTCAGTGGC 186
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QY 187 AGTGGGTCTGGGACAGAAATTCATCTCACCATCAGCAGCCTGCAGTCGAGGACTTTTGCA 246
Db 253 gtttattactgcagcagtaataactggtgcagatcaccttcggcccaaggagac 305
QY 247 GTTTATTCTGTCAACACTATAGTACCTGGCGGCTCAGTTTCGGCGGGGGGAC 299

RESULT 10
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DEFINITION H.sapiens mRNA for immunoglobulin kappa light chain VJ region (ID POM458).
ACCESSION U26909
NID g1359861
KEYWORDS immunoglobulin, immunoglobulin kappa chain, immunoglobulin light chain; joining region; variable region.
SOURCE human
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 393)
AUTHORS Juul, L., Hougs, L., Andersen, V., Svejgaard, A. and Barington, T.
TITLE The normally expressed kappa immunoglobulin light chain gene repertoire. Frequent occurrence of features often assigned to autoimmunity
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 393)
AUTHORS Juul, L.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-1996) Juul L., Dept. of Clinical Immunology KI 7631, Rigshospitalet, National University Hospital, Tagensvej 20, 2200 Copenhagen N, DENMARK
FEATURES
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ORIGIN

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Db 140 ccagtcagagtgtagcacaaccttagcctgggtaccagcagagacacctggccaggtctccc 199
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Db 200 ggcctctcatctatgtgtctccaccagggccactggtatccagcagaggttcagtgcca 259
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QY 188 GGGGTCTGGGACAGAAATTCATCTCACCATCAGCAGCCTGCAGTCGAGGACTTTTGCA 247
Db 320 ttttattactgcagcagtaataactggtgcagatcaccttcggcccaaggagac 379
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Db 380 agatcaa 386
QY 308 AGTTCAA 314

RESULT 11
LOCUS HSU82258 324 bp rRNA PRI 13-JAN-1997
DEFINITION Human anti-ssDNA antibody light chain variable region (Humkv328h5) mRNA, partial cds.
ACCESSION U82258
NID g1773056
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 324)
AUTHORS Suenaga, R.
TITLE Molecular analysis of human anti-ssDNA antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 324)
AUTHORS Suenaga, R.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1996) Immunology Research Laboratory, St. Luke's Hospital, 4400 Wornall Road, Kansas City, MO 64111, USA
FEATURES
    Location/Qualifiers
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            /cell_line="EB virus-transformed human B cell line"
            1..324
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            /gene="Humkv328h5"
            /note="the VKIIa germline gene family"
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            /product="anti-ssDNA antibody light chain variable region"
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BASE COUNT 78 a 90 c 85 g 71 t
ORIGIN

Query Match      74.3%; Score 234; DB 95; Length 324;
Best Local Similarity 88.0%; Pred. No. 9.93e-176;
Matches 271; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Db 13 acgagtcctccagccaccctgtctgtctccaggggaaagccaccctctctgcagg 72
QY 7 ACCAGTCTTCAGCCACCTGTCTGTCTCCAGGGGAAAGAGCTCTCTCTCTCCAGG 66
Db 73 gccagtcagagtgtagcagcaacttagcctgtaccagcagaaacctggccaggtccc 132
QY 67 GCAGTCAGAGTGTCTCGTATACAAATTTAGCTTGTGTATACAGCAAACTTGGCCAGGTCTCC 126
Db 133 aggcctctcatctatgtgtcatccaccagggccactggtatccagcagaggttcagtgcca 252
QY 127 AGGCTCTCATTTATGTGTGGAACACACAGAGCCACTGGTACCCAGACAGAGTTTCAGTGGC 186
Db 193 agtgggtctggagacagagttcactctccaccatcagcagcctgcagctggaagatttgcga 252
QY 187 AGTGGGTCTGGGACAGAAATTCATCTCACCATCAGCAGCCTGCAGTCGAGGACTTTTGCA 246
Db 253 gtttattactgcagcagtaataactggtgcagatcaccttcggcccaaggagac 305
QY 247 GTTTATTCTGTCAACACTATAGTACCTGGCGGCTCAGTTTCGGCGGGGGGAC 299

RESULT 10
LOCUS HSPOM458 393 bp DNA PRI 02-JUN-1996
DEFINITION H.sapiens mRNA for immunoglobulin kappa light chain VJ region (ID POM458).
ACCESSION U26909
NID g1359861
KEYWORDS immunoglobulin, immunoglobulin kappa chain, immunoglobulin light chain; joining region; variable region.
SOURCE human
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 393)
AUTHORS Juul, L., Hougs, L., Andersen, V., Svejgaard, A. and Barington, T.
TITLE The normally expressed kappa immunoglobulin light chain gene repertoire. Frequent occurrence of features often assigned to autoimmunity
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 393)
AUTHORS Juul, L.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-1996) Juul L., Dept. of Clinical Immunology KI 7631, Rigshospitalet, National University Hospital, Tagensvej 20, 2200 Copenhagen N, DENMARK
FEATURES
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BASE COUNT 89 a 121 c 101 g 82 t
ORIGIN

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Best Local Similarity 88.1%; Pred. No. 1.28e-176;
Matches 271; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db 80 ccagtcctccagccaccctgtctgtctccaggggaaagccaccctctctgcagg 139
QY 8 CCAGTCTTCAGCCACCTGTCTGTCTCCAGGGGAAAGAGCTCTCTCTCTCCAGG 67

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QY 127 AGGCTGCTCAATTAAGTGGTAAATATACAGTCACTATTAATGAGGACATACATATGATAATGATAATACATGAT 186
DB 193 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 252
QY 187 AGTGGGTGGGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 246
DB 253 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
QY 247 GTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 306
DB 313 GAAATCA 320
QY 307 AGATTCAT 314

RESULT 12
LOCUS HUMIGLVAA 327 bp mRNA PRI 07-JUN-1994
DEFINITION Human clone 0-16VL immunoglobulin light-chain mRNA V-J region, partial cds.
ACCESSION L19906
NID g348203
KEYWORDS immunoglobulin light chain; joining region; variable region
SOURCE Homo sapiens cDNA to mRNA
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 327)
AUTHORS Sasano,M., Burton,D.P. and Silverman,G.J.
TITLE Molecular selection of human antibodies with an unconventional bacterial B cell antigen
JOURNAL 7 Immunol 151 (12): 5822-5929 (1993)
MEDLINE 94044806
AUTHORS Silverman,G.J.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1993) G.J. Silverman, Sam and Rose Stein
Institute for Research on Aging, University of California at San
Diego, La Jolla, CA 92093, USA
FEATURES
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/tissue="liver"
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/db_xref="PIR:g348204"
/translation="MAPLTGSPILSVSPSPERATLSCPASQSVNNLAWYQKSGQAP
RLIYGASTATGIPAPFGSGSGEIIAIGLSLSEFAVYQRYNNWPFSSFGG
TKLEIKR"
BASE COUNT 73 a 98 c 85 g 71 t
ORIGIN
Query Match 74.3% Score 234: DB 99: Length 327:
Best Local Similarity 92.1% Pred. No. 9.93e-176:
Matches 255: Conservative 0: Mismatches 22: Indels 0: Gaps 0:

DB 7 GAGCTGCTCAATTAAGTGGTAAATATACAGTCACTATTAATGAGGACATACATATGATAATGATAATACATGAT 66
QY 1 GAGCTGCTCAATTAAGTGGTAAATATACAGTCACTATTAATGAGGACATACATATGATAATGATAATACATGAT 60
DB 67 TACAGGCTGCTCAATTAAGTGGTAAATATACAGTCACTATTAATGAGGACATACATATGATAATGATAATACATGAT 126
QY 61 TACAGGCTGCTCAATTAAGTGGTAAATATACAGTCACTATTAATGAGGACATACATATGATAATGATAATACATGAT 120
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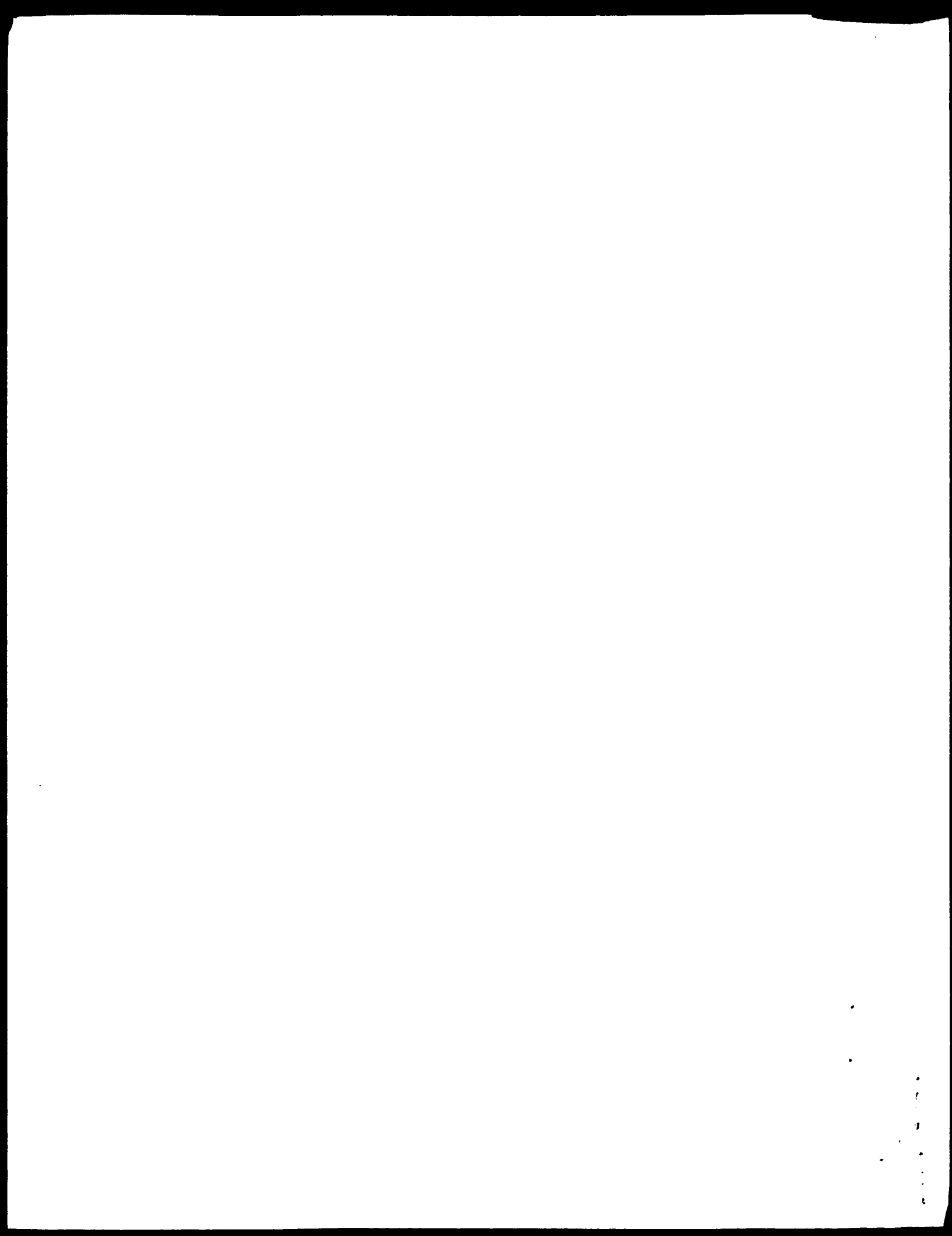
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QY 241 TTTGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 278

RESULT 13
LOCUS HUMIKCVI 321 bp mRNA PRI 02-MAY-1996
DEFINITION Homo sapiens (clone PAG21B) Ig kappa chain mRNA, V-region, partial cds.
ACCESSION L37309
NID g845533
KEYWORDS immunoglobulin light chain; kappa-immunoglobulin; variable region.
SOURCE Homo sapiens (clone: PAG21B) cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Ohlin,M., Sundqvist,V.A., Mach,M., Wahren,B. and Borrebaeck,C.A.
TITLE Fine specificity of the human immune response to the major neutralization epitopes expressed on cytomegalovirus gp58/116 (UH) as determined with human monoclonal antibodies
JOURNAL J. Virol. 67 (2): 703-710 (1993)
MEDLINE 93124562
AUTHORS Ohlin,M., O'Garra,H., Mach,M. and Borrebaeck,C.A.
TITLE Light chain shuffling of a high affinity antibody results in a drift in epitope recognition
JOURNAL Mol. Immunol. 33 (1): 47-56 (1996)
MEDLINE 96174997
FEATURES
Source Location/Qualifiers
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<1..321
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BASE COUNT 74 a 94 c 83 g 70 t
ORIGIN
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Best Local Similarity 87.7% Pred. No. 5.98e-174:
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DB 13 AGGCTGCTCAATTAAGTGGTAAATATACAGTCACTATTAATGAGGACATACATATGATAATGATAATACATGAT 72
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DB 73 GAGCTGCTCAATTAAGTGGTAAATATACAGTCACTATTAATGAGGACATACATATGATAATGATAATACATGAT 180

```

WQERLEH

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MPsearch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 09:02:42 1998 Maspar 1000 100 50 seconds
Tabular output not generated.
Title: >US-08-844-215-17
Description: (118) from US08844215 seq
Perfect Score: 319
N A Sequence: : TACCTTCACTTATCTCTAGG : GAGCTAAGTTTCTAATATAAA 118
Comp: CTGGATGCTGTAGAGAGGTCCT : GCTTTCGCTCAAGCTTCTAGTTT

Scoring table: TABLE default
Gap 5
Nmatch STD Dbase 0: Query 0
Searched: 397346 seqs, 141010104 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

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7: EST203 8: EST204 9: EST205 10: EST206 11: EST207 12: EST208
13: EST209 14: EST210 15: EST211 16: EST212 17: EST213
18: EST214 19: EST215 20: EST216 21: EST217 22: EST218
23: EST219 24: EST220 25: EST221 26: EST222 27: EST223
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119: EST315

Statistics: Mean 9.839; Variance 1.925; scale 5.110
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Prod. No.
1	266	83.6	400	116	AA456778	247711111 Soares ova 0.00e+00
2	255	80.2	346	26	AA300582	EST13427 Testis tumor 0.00e+00
3	249	78.3	349	59	AA379044	EST91999 Skin tumor 0.00e+00
4	242	76.1	403	73	AA345486	EST51505 Gall bladder 0.00e+00
5	237	74.5	402	52	AA350223	EST59341 Lymph node 0.00e+00
6	227	65.1	328	24	AA295311	EST100471 Pancreas tu 0.00e+00
7	193	60.7	370	24	AA295093	EST100400 Pancreas tu 0.00e+00
8	186	58.5	363	55	AA367405	EST78511 Pancreas tum 0.00e+00
9	182	57.2	277	24	AA295377	EST100538 Pancreas tu 0.00e+00
10	178	56.0	284	37	AA327218	EST30585 Colon I Homo 0.00e+00
11	177	55.7	253	25	AA295941	EST101165 Thymus II: 0.00e+00
12	174	54.7	294	55	AA366461	EST77408 Pancreas tum 0.00e+00
13	173	54.4	264	24	AA295154	EST100323 Pancreas tu 0.00e+00
14	161	50.6	269	87	AA434001	240550111 Soares ova 1.04e-171
15	147	48.3	269	100	AA243560	240212111 Soares ova 1.00e-172
16	146	45.9	283	53	AA361678	EST70983 T-cell lymph 1.04e-170
17	145	45.5	209	100	AA292499	EST3011211 Soares ova 1.04e-173
18	142	44.7	238	62	AA383014	EST97987 Thymus II: Ho 3.16e-172
19	135	42.5	260	71	AA225858	nc376051111 Not CGAF P 9.01e-178
20	134	39.0	230	97	AA434180	nc376110111 Soares ova 3.56e-195
21	134	39.0	243	83	AA432182	24111061111 Soares ova 3.00e-195
22	134	39.0	243	83	AA434594	24111061111 Soares ova 3.00e-195
23	134	39.0	244	86	AA430565	24111061111 Soares ova 3.00e-195
24	132	38.4	255	99	AA284552	EST4031111 Soares ova 4.39e-191
25	132	38.4	323	26	AA300732	EST13847 Testis tumor 1.49e-191
26	132	38.4	345	39	AA335086	EST94457 Esophagus tu 4.39e-191
27	130	37.7	257	100	AA291691	2409e10111 Soares ova 5.87e-185
28	119	37.4	255	100	AA292047	2409e10111 Soares ova 5.87e-185
29	118	37.1	433	37	AA301347	EST14079 Testis tumor 6.42e-183
30	116	36.5	335	33	AA318377	EST20620 Spleen I Hom 7.61e-179
31	114	35.8	352	27	AA301461	EST14181 Testis tumor 8.99e-175
32	112	35.2	249	79	AA402152	24050951111 Soares ova 1.02e-170
33	109	34.3	357	53	AA361497	EST71040 T-cell lymph 1.22e-164
34	107	33.6	442	80	AA405415	24056021111 Soares ova 1.35e-160
35	106	33.3	382	25	AA295786	EST100987 Pancreas tu 1.41e-158
36	104	32.7	232	72	AA320371	24132041111 Not CGAF P 1.52e-154
37	102	32.1	374	37	AA327254	EST70547 Colon I Homo 1.00e-150
38	99	31.1	363	26	AA300051	EST13704 Testis tumor 1.08e-144
39	96	30.2	303	26	AA300789	EST13748 Testis tumor 1.04e-138
40	96	30.2	398	94	AA423447	24030031111 Soares ova 1.08e-148
41	95	29.9	240	92	AA419046	24030031111 Soares ova 1.07e-146
42	95	29.9	248	85	AA430449	24030111111 Soares ova 1.07e-146
43	95	29.9	303	26	AA300821	EST14011 Testis tumor 1.07e-146
44	95	28.9	329	33	AA318429	EST2008 Spleen I Hom 1.07e-130
45	91	28.5	329	37	AA327357	EST10702 Colon I Homo 1.02e-129

ALIGNMENTS

RESULT 1
LOCUS AA456778 400 bp mRNA
DEFINITION 247711111 Soares ova tRNA NEHC1 Homo sapiens ova 1180 nt (1994)
DEFINITION 247711111 Soares ova tRNA NEHC1 Homo sapiens ova 1180 nt (1994)
(HUMAN)
ACCESSION AA456778
NID Q2177199
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotic; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubaque, I., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, M., Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theisinger, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE WashU-Merck EST Project 1997

JOURNAL COMMENT Unpublished (1997)

Contact: Wilson PK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St Louis, MO 63109
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

This clone is available royalty-free through LNL : contact the
IMAGE Consortium (infoimage@lml.gov) for further information.
Trace considered overall poor quality
Seq primer: -28ml3 rev2 Est from Amersham
High quality sequence step: 1
Location/Qualifiers
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TGTACCAATCTGAAGTGGAGGGCGGGTTTTTTTTTTTTTTT 3']
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(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
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Matches 292; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

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Db 130 ggcagtcacagtggttagcagcagctgcttagcctgggtaccagcagaacccctgccagct 189
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QY 67 GCGAGTCACAGCTTTAGGAGCACTACTTAGCTTGGTACCAGCAAAAACCTGGCAGGCT 126
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Db 190 cccagctctctatctatgtgtgcatccagcaggggcaactggcatccagcaggttcagt 249
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QY 127 CCGAGGCTCTCATCTATGCTGTATCCAGCAGGGGCTCATGCTCCAGAGAGGTTTCAGT 186
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Db 250 gcaagtggtctgaacagagcttcaactcaacatcgagcagagctggagcctaacattt 309
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Db 310 tgcagtgattactctcagcagcttcaactcaacatcgagcagagctggagcctaacattt 369
|||||
QY 245 TGCAGTGTATTACTCTCAGCAGTATGTTAGTGTACCTCAGCTCTTGGCCAGGGGACCAA 305
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Db 370 ggtggaaatcaaa 382
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QY 306 GTTGGAGATCAAA 318
|||||

RESULT 2
LOCUS AA300582 346 bp mRNA EST 18-APR-1997
DEFINITION EST13427 Testis tumor Homo sapiens cDNA 5' end similar to
immunoglobulin kappa light chain, VJ regions
ACCESSION AA300582
NID q19529.25
KEYWORDS EST.
SOURCE human

ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.

REFERENCE
AUTHORS
1 (bases 1 to 346)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man, W.-L.C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodak, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkley, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-L., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Peilgrino, S.M.,
Phillips, C.A., Pyder, S.E., Scott, J.L., Saudak, D.M., Shirley, P.,
Small, K.V., Spriggs, T.A., Unterhark, T.P., Weidman, J.F., Li, Y.,
Bednarek, D.P., Gao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-P., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.

TITLE
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL
MEDLINE
COMMENT
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other_ESTS: THC169106
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
Seq primer: M13 Reverse

FEATURES
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ORIGIN

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Best Local Similarity 91.9%; Pred. No. 0.00e+00;
Matches 282; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

Db 34 ctccagcagccctgtnttttttccaggggaagagccacctctctcagggccatn 93
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QY 14 CTCAGGACACCTCTTCTCTCTCCAGGCAAGAGCACTCTCTCTCTCTCTCTCTCT 73
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Db 94 agagtgttagcagcagcttagcctggtaccagcagaaacctagccaggtcccaagc 153
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QY 74 AGAGTGTTAGGAGCAACACACACACACACACACACACACACACACACACACAC 133
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Db 154 tctnattctatggtgcatccagcagggccactggcctccacacaggttcagtgcautg 213
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QY 134 TCCCTCATCTATGCTGTATCTCAGGAGGCCACTGGCATCCACAGAGGTTTCAGTGG 193
|||||

Db 214 gctctggagcagacttccactctcaccatccagcagcagcagcagcagcagcagcag 273
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QY 164 GGTCTGGGAGAGAGATTCACTTCACTCACTCACTCACTCACTCACTCACTCACT 252
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Db 274 tattactgtcagcagctatggttagctcancctgagcaggttcgcccaggaagcagctag 333
|||||
QY 253 TATTACTGTCTAGCAATATGTAATCACTCACTCACTCACTCACTCACTCACTCA 311
|||||

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9712 Medical Center Drive
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For clone availability,
see www.tigr.org

Kozak, D. L., Kinsch, C., Hung, J., Li, H., Weisner, P. S., Olsen, H., Raymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, C. L., Rubin, S. M., Thompson, L. P., Fannon, M. H., Rosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M. and Venter, J. C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence. *Nature* 377 (6547 Suppl.), 3-174 (1995)

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For clone availability, additional sequence and expression
information related to this EST, please check the IGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M3 Reverse
Location/Qualifiers

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0.978  

/organism="Homo sapiens"  

/note=Organ. pancreas. Vector. pBluescript SK-. Site1:  

Eccefi. Site2. XhoI.  

/clonelib=Pancreas tumor I"  

/dev_stage="adult"  

<1..>370  

      65 a   107 c    94 y    77 t     7 others  
  

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Similarity 88.8%: Pred No.0.00e+00:  

231: Conservative 0: Mismatches 26: Indels 3: Gaps 11:  
  

gcannttccagcgcacccctgccgtatncccaggggaaaagaccacctctctcttcad tta  

TGCAGTCGCCAGGACCCCTGTCTTGTCATCAGGGCAAAAGATATCGCTCTCTTTGGG GA  

caattcacagtctttacacaact ---tagcctgtaccagcagaataatcgaccagaa 175  

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|||  

AATCATAGAGTGTATTAGAGCACACTATTAAGCTTGGTAGAGAAAAGCTTGGCT TAGGCT 126  

cagcgtcccatnatcttatnattgatccacagggccaactggtatccccagccaatctcaat 235
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ccgctgggtctgggcagagatttcactcctctaccatccacgccagcctacacattcgaaattct 245
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CACTATCGTGTGGGAGACAGATTCACTTCATCATCATCAGTAACTATGAGAGCTTGAGATTTT 246
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agtttattactctcagca 315
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ACTGTAATACTGTCAGCA 266
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AA367405 363 bp rRNA EST 21 APR 1997
EST78511 pancreas tumor III Homo sapiens cDNA 5' end similar to
similar to immunoglobulin kappa light chain.

AA367405
92016753
EST.
human.
Homo sapiens
Eukaryotes, mitochondrial eukaryotes, Metazoa; Chordata:
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
1 (bases 1 to 363)
Adams, M. D., Krujavage, A. P., Fleischmann, R. D., Fuldner, H. A.,
Bult, C. J., Lee, N. H., Kirkness, E. F., Watson-Rock, K. G., Beckman, J. D.,
White, G., Sutton, G., Blake, J. A., Brandon, P. C., Man-Wai, C.,
Clayton, P. A., Gilpin, T. B., Cotton, M. P., Earle-Hughes, E., Fine, L. I.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodex, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, I.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280

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Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
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/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1:
EcoRI; Site: 2: XhoI"
/clone_lib="Pancreas tumor III"
/dev_stage="adult"
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ORIGIN
mpna
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Query Match 58.5%; Score 186; DB 55; Length 363;
Best Local Similarity 82.9%; Pred. NO. 0.00e+00;
Matches 252; Conservative 0; Mismatches 49; Indels 3; Gaps 3;

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QY 14 CTCAGGACCCCTGCTTGTTCAGGAGGAGAGAGGACCCCTCTCTCTGCGGGGCTAGTC 73

Db 61 agagtttgta-cgt-t-cttagcctgtatcagcacaaacctggccaaacctccagcc 117
QY 74 AGAGTGTAGGAGCACTACTTAGCTGTGTACGACCAAAACCTGGCCAGGCTCCCAAGC 133

Db 118 tctcatcatagtggtgtccacagggccactgtactccggccacacctcagtgagcggtg 177
QY 134 TCTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 193

Db 178 ggtctagagcaaatcactctccaccatcagcgccctcagctcgtgagacctttgagctat 237
QY 194 GGTCTGGGACACATCTACTCTCACCATCAGCAGACTGGACCTGAAGATTTTGACGTGT 253

Db 238 actattgtagagtagtatataactgacctctcacttttcggcgaggagaccacagtagaga 297
QY 254 ATTACTGTGAGGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 313

Db 298 teaa 301
QY 314 TCAA 317

RESULT . 9
LOCUS AA295377 277 bp mRNA EST 18-APR-1997
DEFINITION EST100538 Pancreas tumor I Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VJ regions.

AA295377
gi1947711
EST
human
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1. (bases 1 to 277)
Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fulgner, P.A., Rult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodex, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, I.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280

COMMENT
Other ESTs: THC169106
Contact: Kerlavage, AR
Bioinformatics
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Fax: 3018699423

Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
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/organism="Homo sapiens"
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EcoRI; Site: 2: XhoI"
/clone_lib="Pancreas tumor I"
/dev_stage="adult"
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FEATURES
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BASE COUNT
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mRNA
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Best Local Similarity 93.8%; Pred. No. 6.00e-06;
Matches 196; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Db 70 acgagcttcagagccacctgtttgttccagggggaagagagccacctctcagagag 129
QY 7 ACCGAGTCTCAGGACCCCTCTTTGTCTCCAGGGAAGAGAGAGAGAGAGAGAGAGAG 66

Db 130 gccagtcagagtgtagcagcagctacttagcctggtaccagagaaacctcagcagct 189
QY 67 GCCAGTCAGAGTGTAG 126

Db 190 cccagntccctcatctatgctcagagggcagcagctggnatccacagaggttcagt 249
QY 127 CCCAGGCTCCTATCTATGTTGTTATCCAGGAGGAGAGAGAGAGAGAGAGAGAG 186

Db 250 ggcagtggtgctgggacag-cttcactct 277
QY 187 GGCAGTGGGCTCGGCAGACAGACTTTCACCTCT 215


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RESULT 10
LOCUS AA127218 289 bp mRNA EST 20-APR-1997
DEFINITION EST127218 Homo sapiens cDNA 5' end similar to similar to
immunoglobulin kappa light chain, VJ regions (GB:211894).
ACCESSION AA127218
NID g1979524
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 289)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,P.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gageyone,D.,
White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C.,
Clayton,R.A., Cline,T.P., Cotton,M.D., Earle-Hughes,E., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Pyder,S.E., Scott,J.L., Saudok,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,F.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olson,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yang,L., Ruben,S.M.,
Dillon,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M., and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE 96026280
COMMENT
Contact: Kerlavage, AR
Bioinformatics
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Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tigrdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES
Location/Qualifiers
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/notes="Organ: thymus; Vector: phagescript SK-; Site:1"
EcoRI, Site:2: XhoI"
/clone.lib="Colon I"
/dev_stage="adult"
BASE COUNT 56 a 88 c 73 g 59 t 3 others
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Best Local Similarity 91.3%; Pred. No. 0.00e+00;
Matches 200; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

Db 72 gctgaagcag-ctccagagcaccctatncttcttccagaggggagagagcaccctctctg 130
QY 3 gctcagcagcttcagagcaccctctcttcttcttcttcttcttcttcttcttcttctt 52

Db 131 caggaccagctcagagcttcttcttcttcttcttcttcttcttcttcttcttcttctt 190
QY 63 cgggctcagctcagagcttcttcttcttcttcttcttcttcttcttcttcttcttctt 122

Db 191 gctctcagagctcagagcttcttcttcttcttcttcttcttcttcttcttcttcttctt 250
QY 123 cggctcagagctcagagcttcttcttcttcttcttcttcttcttcttcttcttcttctt 182

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Db 251 cagtcagcagctgagctgagctgagcagcagcagcagcagcagcagcagcagcagcagcagc 289
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RESULT 11
LOCUS AA205941 253 bp mpNA EST 18-APR-1997
DEFINITION EST011165 Thymus III Homo sapiens cDNA 5' end similar to similar to
immunoglobulin kappa light chain, V region (GB:Y00440).
ACCESSION AA205941
NID g1948286
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 253)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,P.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gageyone,D.,
White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C.,
Clayton,R.A., Cline,T.P., Cotton,M.D., Earle-Hughes,E., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Pyder,S.E., Scott,J.L., Saudok,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,F.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olson,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yang,L., Ruben,S.M.,
Dillon,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M., and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
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COMMENT
Contact: Kerlavage, AR
Bioinformatics
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tigrdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES
Location/Qualifiers
source
1..253
/organism="Homo sapiens"
/notes="Organ: thymus; Vector: phagescript SK-; Site:1"
EcoRI, Site:2: XhoI"
/clone.lib="Thymus III"
/dev_stage="adult"
BASE COUNT 63 a 69 c 55 g 53 t 3 others
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Best Local Similarity 87.5%; Pred. No. 0.00e+00;
Matches 203; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 1 cagcagcagctgagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 60
QY 87 cagcagcagctgagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 146

Db 61 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120
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QY 147 TGTATCCAGCAGGCGCCATGGCATCCAGACAGAGGTTTCAGTGGAGTGGGTCTCTGGGACAGA 206
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 QY 207 CTTCCTACTCTCACCATCAGCAGACTGGAGCTGAGATGTTTTCAGTGTATTACTGTTCAGCA 266
 Db 181 gtataaactgagcagagagagcttcggccaaaggaccagagtggaatcaaa 232
 QY 267 GTATGTTAGTCACTCAGCTCGGACTTTTGGGCGAGGGGACCAAGTTGGAGATCAAA 318

RESULT 12 AA366461 294 bp mRNA EST 21-APR-1997
 LOCUS EST77408 Pancreas tumor III Homo sapiens cDNA 5' end similar to
 DEFINITION similar to immunoglobulin kappa light chain, V region.
 ACCESSION AA366461
 NID G2018779
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata:
 Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea:
 Homo.

REFERENCE 1 (bases 1 to 294)
 AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, P.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
 Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, P.,
 Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, T.A., Collins, E.J.,
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, J.A., Collins, E.J.,
 Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S., Kim, A.K.,
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
 Dillion, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M., and Venter, J.C.
 TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 96026240
 COMMENT Other ESTs: THC168243
 Contact: Kerlavage, AR
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 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
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 EcoRI; Site_2: XhoI"
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 Best Local Similarity: 92.2%; Prob No. 6.67e-269;
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Db 85 acgcaatctcagacacacccctgtgtctctccaggggaagacccaccctctctcaggg 144

QY 7 ACCGAGTCTCCAGGACACCTGCTGTTTGTCTCCAGGGAAGAGACACCTGCTGCTGAGG 66
 Db 145 gccagtnagaagtttaggagaaactacttagctgaactccacagaaataaaccaagct 204
 QY 67 GCCAGTCAGAGTGTTAGGAGCAACTACTTAGCTGGTACCCAGCAAAACCTGGCCAGGCT 126
 Db 205 cccaggctctcatctatgtatctccaccagggccagtggtgtccacccaagtctcagt 264
 QY 127 CCCAGGCTCTCATCTATGCTGATCCAGCAGGGCCACTGGCATCCACACAGAGTTCAST 186
 Db 265 gccagtgaggctcgggacagaaattca 289
 QY 187 GGCAGTGGGCTCTGGGACAGACATTC 211

RESULT 13 AA295154 264 bp mRNA EST 18-APR-1997
 LOCUS EST100323 Pancreas tumor I Homo sapiens cDNA 5' end similar to
 DEFINITION immunoglobulin kappa light chain, VJ regions.
 ACCESSION AA295154
 NID G1947509
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata:
 Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea:
 Homo.

REFERENCE 1 (bases 1 to 264)
 AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, P.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
 Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, P.,
 Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, T.A., Collins, E.J.,
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, J.A., Collins, E.J.,
 Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P.S., Kim, A.K.,
 Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
 Dillion, P.J., Fannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M., and Venter, J.C.
 TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 96026280
 COMMENT Other ESTs: THC169106
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 Location/Qualifiers
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 EcoRI; Site_2: XhoI"
 /clone_lib="Pancreas tumor I"
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 ORIGIN

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Matches 166: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

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      |||||
QY      7  AGCGAGTCTCCAGAGACCTGTGTTTGTCTAGAGGGAAAGAGACACCTCTCTGTGGGG 66

Db      159  gccagtcacagatggttagcagcagctacctagcctagtaccagggagaaacctgggcacct  214
      |||||
QY      67  GTCAAGTCACAGTGTAGAGAGAACTAGCTTGTGTACTAGTAAAAAATCTGSCACGTT  124

Db      219  ccagactctctcatctataggtgtcatctccagggggccactgtgcatctcccaaac  269

QY      127  CCAGAGGCTCTCATATATGTTGTTGATCTCCAGAGAGGGTACTGTGATCTCCAGAC  177

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LOCUS	209 bp	mRNA	EST
DEFINITION	279942.r1 Soares ovary tumor	NRHOT Homo sapiens	CNA clone 72742
DEFINITION	5' similar to gr-X6764	IG KAPPA CHAIN PRECURSOR	VIII REGION (HUMAN):

ACCESSION	REFERENCE	TITLE
NID	AUTHORS	JOURNAL
KEYWORDS		COMMENT
SOURCE		
ORGANISM		

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4414 Forest Park Parkway, Box 9501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through ILM : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
1 209

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mRNA
BASE COUNT
ORIGIN
Query: Mat
Best Local
Matches

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Db 47 ctccaggcaccctgtcttctccagggqaaagagccaccctctctctgagggccagtc 106
QY 14 CTCAGGACCCCTGTCTTTGTCTCCAGGAGAAAGAGCCACCTCTCTCTGCGGACAGTC 73
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Db 167 tctcatctatggtgcctccagcagggccactgg-atcccagac 209
QY 134 TCCTCATCTATGCTGTATCCAGCAGGCGCCACTGGCATCCAGAC 177

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Search completed: Tue Feb 24 08:05:25 1998
 Job time : 162 secs.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chondata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 381)

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Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

TITLE
JOURNAL
COMMENT

CONTACT: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).

FEATURES
source
Location/Qualifiers
1..381
/organism="Homo sapiens"
BASE COUNT 86 a 109 c 97 g 86 t 3 others
ORIGIN
Query Match 79.6%; Score 253; DB 58; Length 381;
Best Local Similarity 93.2%; Pred No. 0.00e+00;
Matches 275; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
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QY 14 CTCACGGCACCTGTCTTGTCTCCAGGGGAAAGAGCCACCTCTCTCTGCGGGGCCAGTC 73
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Db 207 tctctatctatgatgatctccacagagggccgctggcctccacagagattcactggcagtg 266
QY 134 TCCATCATTATGTTGTTATCCAGAGGCGACCTGGCATCCCAAGAGTTCAGTGGCAATG 193
Db 267 ggtctgggacagacttcacttcacatcagcagacttgagacctgaagatttttgcagtg 326
QY 194 GGCTGGGACAGACTTCACCTTCACCATCAGCAGACT-GGAGCCCTGAAGATTTCAGCTG 252
Db 327 tatnctgtcagcagctatgtatgtacactctgttaatttttgncaaggagaccagct 381
QY 253 TATTACTGTACAGATATGTTAGCTTCACTCGGACTTTTGGCCAGGGGACCAACT 307

RESULT 2
LOCUS T29916 383 bp mRNA EST 06-SEP-1995
DEFINITION EST99871 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
light chain, V region (GB:M27025) (HT:3778).

ACCESSION T29916

g612014
EST.
human primer=M13 Reverse library=Human Pancreas.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chondata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
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YU, G.-L., RUBEN, S.M., DILLON, P.J., FANNON, M.P., ROSEN, C.A.,
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Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

TITLE
JOURNAL
COMMENT

CONTACT: Venter, JC
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932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).

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source
Location/Qualifiers
1..383
/organism="Homo sapiens"
BASE COUNT 88 a 105 c 98 g 88 t 4 others
ORIGIN
Query Match 77.7%; Score 247; DB 59; Length 383;
Best Local Similarity 91.1%; Pred No. 0.00e+00;
Matches 286; Conservative 0; Mismatches 25; Indels 3; Gaps 3;
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QY 127 CCCAGGCT 186
Db 231 ggcagtggtctggagcagacttctcaactcttgaccatcagcagactggagctgaagatt 290
QY 187 GGCAGTGGGCTCTGGGAGAGACTT-CACTCTCTCTCTCTCTCTCTCTCTCTCTCT 244
Db 291 ttgcagctgtattactgtcagcagctatgttagctctccggggagagcttcggagagagc 350
QY 245 TT-GCAGTGTATTACT 303
Db 351 aaggtggaagatcaa 364
QY 304 AAGTTGGAGATCAA 317

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	127870	EST19007 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain V region (GB:X05763) (H1:30873).	127870	45034568	EST	human primer-M13 Reverse library-Human Lung.	Eukaryotes	1 (bases 1 to 383)	Adams, M. D., Kerlavage, A. P., Fleischmann, P. D., Fuldner, P. A., White, C. J., Sutton, N. J., Kinknes, E. F., Weinstock, K. C., Gocayne, J. D., Bult, C. J., Linton, G., Blake, J. A., Brandon, R. C., Chui, M. W., Clayton, R. A., Cline, R. T., Cotton, M. D., Earle-Hughes, J., Fine, L. B., FitzGerard, L. M., Fritch, W. M., Fritch, L., Goughagen, N. S. M., Glodde, A., Gnehm, C. I., Hanna, M. C., Hedblom, E., Hinkle, J. P. S., Kelley, J. M., Kline, K. M., Kelley, J. C., Liu, L. I., Marmaro, S. M., Merrick, J. M., Moreno-Palacios, P. F., McDonald, L. A., Nguyen, D. T., Pelletier, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Utterback, J. K., Saudek, D. M., Shirley, P., Small, K. V., Springs, J. A., Tagherback, J. K., Coleman, J. A., Collins, E. J., Bodnarik, D. P., Cao, L., Cepeda, M. A., Weisman, T. F., Collins, E. J., Dirke, D., Feng, P., Ferris, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J. C., Hudson, P., Kim, A., Kozak, D. L., Kunsch, C., Li, H., Li, H., Messner, P. S., Olsen, H., Raymond, L., Wei, Y. F., Wing, J. C., Xu, C., Yu, G. L., Ruben, S. M., Dillon, P. J., Fannon, M. P., Posen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.	Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence	Unpublished (1995)	Other ESTs: THC24452
2	127870	EST19007 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain V region (GB:X05763) (H1:30873).	127870	45034568	EST	human primer-M13 Reverse library-Human Lung.	Eukaryotes	1 (bases 1 to 383)	Adams, M. D., Kerlavage, A. P., Fleischmann, P. D., Fuldner, P. A., White, C. J., Sutton, N. J., Kinknes, E. F., Weinstock, K. C., Gocayne, J. D., Bult, C. J., Linton, G., Blake, J. A., Brandon, R. C., Chui, M. W., Clayton, R. A., Cline, R. T., Cotton, M. D., Earle-Hughes, J., Fine, L. B., FitzGerard, L. M., Fritch, W. M., Fritch, L., Goughagen, N. S. M., Glodde, A., Gnehm, C. I., Hanna, M. C., Hedblom, E., Hinkle, J. P. S., Kelley, J. M., Kline, K. M., Kelley, J. C., Liu, L. I., Marmaro, S. M., Merrick, J. M., Moreno-Palacios, P. F., McDonald, L. A., Nguyen, D. T., Pelletier, S. M., Phillips, C. A., Ryder, S. E., Scott, J. L., Utterback, J. K., Saudek, D. M., Shirley, P., Small, K. V., Springs, J. A., Tagherback, J. K., Coleman, J. A., Collins, E. J., Bodnarik, D. P., Cao, L., Cepeda, M. A., Weisman, T. F., Collins, E. J., Dirke, D., Feng, P., Ferris, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. S., Greene, J. M., Gruber, J. C., Hudson, P., Kim, A., Kozak, D. L., Kunsch, C., Li, H., Li, H., Messner, P. S., Olsen, H., Raymond, L., Wei, Y. F., Wing, J. C., Xu, C., Yu, G. L., Ruben, S. M., Dillon, P. J., Fannon, M. P., Posen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C.	Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence	Unpublished (1995)	Other ESTs: THC24452
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Db   318 gtattactgtcagcatatgataac 341
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QY   252 GTATTACTGTCAAGCAGTATGTTAG 275

RESULT 4
LOCUS P70290 570 bp mRNA EST 31-JUN-1995
DEFINITION Y361d8r-f Homo sapiens cDNA clone 155151 S similar to GBX0N764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION P70290
NID 9843807
KEYWORDS NID
SOURCE human clone-155151 library-Scares breast 2NDPRST vector-pIT713P
(Pharmacla) with a modified polylinker host-DNA10B (ampicillin
resistant) primer-MIRBP1 RSite1-Not I RSite2-Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-
TCCTAATCATCGAATGGAGGAGGCCGCCTTTTTTTTTTTTTTTT 3'].
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pIT73 vector (Pharmacla). Library went through one round
of normalizing to a 2x10^7-2x10^8 library concentration by EcoRI
Scares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Channeata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 570)
AUTHORS Hillier,L., Clark,N., Dubouque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,C., Marras,M.,
Parsons,J., Pitkin,L., Rohlfing,T., Soares,M., Tan,P.,
Trevasaki,E., Waterston,P., Williamson,A., Wohlmann,P. and
Wilson,P.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 285 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 316
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL. Contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Location/Qualifiers
source 1..570
Organism="Homo sapiens"
/cloae="155151"
BASE COUNT 122 a 140 c 141 g 149 t 18 others
ORIGIN
Query Match 54.8%; Score 206; DB 34; Length 570;
Best Local Similarity 84.8%. Pred. No. 0.00e+00;
Matches 258; Conservative 0; Mismatches 44; Indels 4; Gaps 4;

Db   93 agcagcttcaggagacctgtttgtctccgggggaagaagaccacctctcccgaaa 152
QY   7 ACAGCTCTCCAGGACACCTTGCTTTTCTTCACGGGAAAGACATCTCTCTCTGCGGG 66

Db   153 tcacgtcaggttgttaacagaaacttcttagcttgatcaccaacaagaacactgtgcagaa 212
QY   67 GCACATCACAGATGTAAGAGAACAACTTATACAGTGGATACACAAAACTAGTAGGCT 124

Db   213 ccccctctctctcatctttgttggtgatccaccagggccactggacatccccacacacttg 272
QY   127 CCACAGGCTCTCTCATCTATATGTTGTATACAGAGGAGGCTATGGATATCCAGATAA 184

Db   273 atggcagtgggtctctggacagactctcactctcaccatccagcagctndagctgaagct 342
QY   185 GTGGCAGTGGGTTGGTGGACACTTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 444

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Db   318 gtattactgtcagcatatgataac 341
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QY   252 GTATTACTGTCAAGCAGTATGTTAG 275

RESULT 4
LOCUS P70290 570 bp mRNA EST 31-JUN-1995
DEFINITION Y361d8r-f Homo sapiens cDNA clone 155151 v similar to GBX0N764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION P70290
NID 9843807
KEYWORDS NID
SOURCE human clone-155151 library-Scares breast 2NBHST vector-pIT73p
(Pharmacla) with a modified polylinker host-DNA10B (ampicillin
resistant) primer-MIRP1 RSite1-Not I RSite2-Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-
TCCTAATCATCGAATGGAGGAGGCCGCTTTTTTTTTTTT 3'].
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pIT73 vector (Pharmacla). Library went through one round
of normalizing to a 2x107-2x108 library consisting of EcoRI
Scares and M.Farina Bonaldo.

ORGANISM
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Channaria; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 570)
AUTHORS Hillier,L., Clark,N., Dubouque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,C., Marras,M.,
Parsons,J., Pitkin,L., Rohlfing,T., Soares,M., Tan,P.,
Trevasaki,E., Waterston,P., Williamson,A., Wohlmann,P. and
Wilson,P.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 285 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 316
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL. Contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Location/Qualifiers
source 1..570
organism="Homo sapiens"
/cclone="155151"
BASE COUNT 122 a 140 c 141 g 149 t 18 others
ORIGIN
Query Match 54.8%; Score 206; DB 34; Length 570;
Best Local Similarity 84.8%. Pred. No. 0.00e+00;
Matches 258; Conservative 0; Mismatches 44; Indels 4; Gaps 4;

Db   93 agcgcagtccaggagaccctgtttgttcgggggggaagaagcacacctctcccggaa 152
QY   7 ACGCAGTCTCCAGGACACCTTGCTTTTCTCCAGGGAAGAAGCACCTCTCTCTGCGGG 66

Db   153 tcacgtcaggttgttaacagacaactctttagcttgatcccaaacaaaacactgtgacagaa 212
QY   67 GCACATCASAGTGTGTAAGAGAACAACTTATACCTGGTAGTACCAAAAACTGGTAGGCT 124

Db   213 cccccctctctctcatctttgttggtgatccaccagggccactggacatctccaacacttng 272
QY   127 CCCAGGCTCTCTCATCTATATGTTGTATCCAGAGGAGGCTATGGGATACCAAGATAAT 184

Db   273 atggcactgggtctcggaacagactctcactctcaccatccagcagactnagactgaagatt 342
QY   185 GTGGCAGTGGGTTGGTGGACAACATCTTCACTTCACTCACTCACTCACTCACTCACTCACT 444

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Db 333 ttgcagtgattactgttcagcagatattgatgggtcancctcttttnggcccctggagcc 392
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QY 245 TTGCAGTGATTACTGT-CAGCAGTAGTGTAGTCTCAGCTCGGACTTTTGGCCAGGGGACC 303
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Db 393 acagtgagaataaaaa 408
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 304 A-AGTTGGAGATCAAA 318
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RESULT 5
LOCUS R10529 401 bp mRNA EST 06-APR-1995
DEFINITION Yf3la06.r1 Homo sapiens cDNA clone 128434 5', similar to gb:X06764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
R10529
NID 9762485
KEYWORDS EST
SOURCE human clone-128434 library=Soares fetal liver spleen INFLS
vector-pT73D (Pharmacia) with a modified polylinker host-DH10B
(ampicillin resistant) primer=M13P1 Psite1=Pac I Psite2=Eco RI
Liver and spleen from a 20 week-post conception male fetus; 1st
strand cDNA was primed with a Pac I - oligo(dT) primer [5',
AAGTGGGAATTAATTAAGATCTTTTTTTTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
Homo sapiens
ORGANISM
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 401)
REFERENCE
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,P., Williamson,A., Wohlmann,P. and
Wilson,P.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 239
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Source
1..401
/organism="Homo sapiens"
/clone="128434"
BASE COUNT 86 a 113 c 105 g 96 t 1 others
ORIGIN
Query Match 63.8%; Score 203; DB 40; Length 401;
Best Local Similarity 92.1%; Pred No. 0.00e+00;
Matches 293; Conservative 5; Mismatches 12; Indels 13; Gaps 13;

Db 74 ctccagagacccctgtattgtatccagaggaagagccacccctctctctgagggccagtc 133
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QY 14 CTCAGAGTACCCCTGTCTTGTCTCCAGAGGAAAGAGCCACCTCTCTCTCTCTCTCTCTCT 73
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Db 134 agagtttagcagcaactacttagctcgttaccagacagaaacctggccaggtccccagg 193
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QY 74 AGAGTGTAGGAGCACTACTTAGCTGTGTAAGAGCAAAACCTTGG-CCAGGCTCCGAGG 132
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Db 194 ctctcatctatgtgtcatccagcagggccactggcattccccadacaggtttcagtgagcag 253
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QY 133 CTCTCATCTATGTTGTATCCAGGAGGCGCATCTGGCAT-CCAGACAGGTTTCAGTGGCAG 191
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Db 254 tgggtctggggacagatttactcttaccattccagcagactggggagacctgaadattttt 313
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QY 192 TGGGTCTGGG-ACAAGATTTACTCT-CAGAT-CAGTACACTGG-AGCTGAAGATTTT- 246
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Db 314 gcagtgattactgttcagcagatattgatgggtcaccgttaccatttctggggcagagaa 373
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QY 247 GCAGTGATT-ACTGT-CAGCAGTAGTGTAGTCTCAGCTCGGACTTTTGGCCAGGGGACC 301
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Db 374 ccaaggttggagatcaaa 391
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 302 CCAAG-TTGGAGATCAAA 318
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RESULT 6
LOCUS H44798 399 bp mRNA EST 31-JUL-1995
DEFINITION YP24a10.r1 Homo sapiens cDNA clone 188346 5', similar to gb:X06764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
H44798
NID 9920850
KEYWORDS EST
SOURCE human clone-188346 library=Soares breast 3NBHst vector-pT73D
(Pharmacia) with a modified polylinker host-DH10B (ampicillin
resistant) primer=M13P1 Rsite1=Not I Rsite2=Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCATCTGAGTGGGAGCGCGCCCTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20 Library constructed by Bento Soares
and M.Fatima Bonaldo.
Homo sapiens
ORGANISM
Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chcanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 399)
REFERENCE
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,P., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 289
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Source
1..399
/organism="Homo sapiens"
/clone="188346"
BASE COUNT 88 a 112 c 104 g 91 t 4 others
ORIGIN
Query Match 61.3%; Score 195; DB 69; Length 399;
Best Local Similarity 92.3%; Pred No. 0.00e+00;
Matches 250; Conservative 0; Mismatches 14; Indels 7; Gaps 7;

Db 70 acgcagctnccagcaccctctgttctccaggtgaaagaccacccctctctctcagc 129
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QY 7 ACGCAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGAGAGAGCTCTCTCTCTCTCTCTCTCT 65
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Db 130 gccagtcagatgtgagcagcaaccaggttagcttggtaccagcaaaacctgaagcagc 189
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QY 67 GCCAGTCAGATGTTAGGAGTAACTTAACTCTGGAACAGTAAAGAACCTGG-CCAGG 125
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[illegible]

Qy 190 ACTGGGTCTGGG 201

Qy 190 AGTGGGTCTGGG 201

Search completed: Tue Feb 24 09:02:18 1998
Job time : 291 secs.

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RESULT 15
LOCUS 51922 361 bp mRNA EST 18-MAY-1995
DEFINITION Y71B07.r1 Homo sapiens cDNA clone 154165 5' similar to
gb:M12740_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN)).
ACCESSION R51922
NID q813824
KEYWORDS EST.
SOURCE human clone=154165 library=Soares breast 2NBHst vector=pf7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13P1 psite1=Not I psite2=Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
IGTACCAATCTGAAGTGGAGGGCGCGCCCTTTTTTTTTTTT 3'].
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 230. Library constructed by Bento
Soares and M.Fatima Bonaldo.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 361)
ILLIER,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,E.,
Trevisan,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

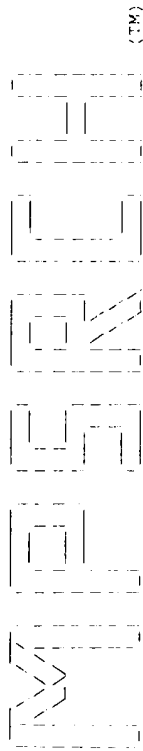
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St Louis MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 308
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
1..361
/organism="Homo sapiens"
/clone="154165"

BASE COUNT 75 a 108 c 91 g 83 t 4 others
ORIGIN
Query Match 41.5% Score 132: DB 28: Length 361:
Best Local Similarity 95.7%: Pred. No. 3,220-212:
Matches 228: Conservative 9: Mismatches 26: Indels 12: Gaps 11:

Db 91 ctccagccaccctctctctctctccgggggaagaatcacccctctctccggagccactc 150
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Gy 14 ctccagccaccctctctctctctccgggggaagaatcacccctctctccggagccactc 73
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Db 151 aagatttttgcgaacacttagcctggttcacagcaaaaacctggggccagctcccaag 207
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Db 208 cctctctctctctctctctctctctctctctctctctctctctctctctctctctctct 267
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Gy 133 ctctctctctctctctctctctctctctctctctctctctctctctctctctctctct 188
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Db 268 cctctctctctctctctctctctctctctctctctctctctctctctctctctctctct 327
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Db 328 tccagctctctctctctctctctctctctctctctctctctctctctctctctctctct 353
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Gy 246 tgcagctctctctctctctctctctctctctctctctctctctctctctctctctctct 270
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

```

21



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MPsrch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 14:06:26 1998: Maspar time 19.72 Seconds
741.630 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-17
Description: (1-318) from USOR44215 seq
Perfect Score: 318
N.A. Sequence: 1 GAGGTACAGGAGTGTTCAGGGGACAAAGTGGAGATCAAA 318
Comp: CTCGAGTGTGTTCAGGATTCCCGCGTTCAGGCTGTAGTTC

Scoring table: TABLE default
Gap %
Nmatch STD : tbase 0: Query 0
Searched: 87531 seqs, 22996021 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
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Statistics: Mean 7.526: Variance 4.259: scale 1.791

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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13	221	59.5	729
14	216	67.9	812
15	212	66.7	900
16	141	44.3	360
17	138	43.4	387
18	131	41.2	339
19	131	41.2	339

20 129 40.6 5239 2 5452363-1 Patent No. 5452363 2,848-75
21 127 39.9 581 6 US-07-634-1 Sequence 82, Applicati 8,396-74
22 127 39.9 581 7 US-08-470-1 Sequence 82, Applicati 8,396-74
23 127 39.9 581 7 US-08-470-1 Sequence 82, Applicati 8,396-74
24 127 39.9 581 7 US-08-470-1 Sequence 82, Applicati 8,396-74
25 126 39.6 333 11 PCT-US93-0 Sequence 8, Applicatio 4,556-73
26 125 39.3 339 11 PCT-US93-0 Sequence 8, Applicatio 4,556-73
27 124 39.0 548 1 5452363-4 Patent No. 5452363 2,848-75
28 123 38.7 339 12 PCT-US93-1 Sequence 82, Applicati 8,396-74
29 123 38.7 339 12 PCT-US93-1 Sequence 82, Applicati 8,396-74
30 123 38.7 339 7 US-08-470-1 Sequence 20, Applicati 7,236-71
31 123 38.7 360 7 US-08-447-1 Sequence 13, Applicati 7,236-71
32 123 38.7 847 7 US-08-053-1 Sequence 184, Applicati 7,236-71
33 123 38.7 1848 7 US-08-447-1 Sequence 15, Applicati 7,236-71
34 123 38.7 5703 7 US-08-470-1 Sequence 50, Applicati 7,236-71
35 123 38.7 5703 7 US-08-470-1 Sequence 50, Applicati 7,236-71
36 123 38.7 5703 13 PCT-US93-1 Sequence 50, Applicati 7,236-71
37 122 38.4 280 7 US-08-300-1 Sequence 52, Applicati 3,916-70
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40 122 38.4 321 10 PCT-US92-0 Sequence 72, Applicati 3,916-70
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42 122 38.4 384 6 US-08-250-1 Sequence 13, Applicati 3,916-70
43 122 38.4 723 7 US-08-425-1 Sequence 89, Applicati 3,916-70
44 122 38.4 723 7 US-08-425-1 Sequence 90, Applicati 3,916-70
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ALIGNMENTS

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DT 01-JAN-1900
DE Sequence 182, Application US/08053131.
CC Sequence 182, Application US/08053131
CC Patent No. 5861016
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patented Release #100, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/000,860
CC FILING DATE: 10-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:


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CC FILLING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA: US 07/826,623
CC APPLICATION NUMBER: US 07/826,623
CC FILLING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILLING DATE: 30-SEP-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILLING DATE: 02-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 646 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHEICAL: NO
CC ANTI-SENSE: NO
CC Sequence 646 BP: 162 A; 187 C; 170 G; 127 T; 0 other;

Query Match      81.4%: Score 259; DB 13; Length 646;
Best Local Similarity 93.1%: Pred No 1 50e-172;
Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Db 1 GAGTTCACGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGAGCCACCTCTCC 60
Qy 1 GAGTTCACGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGAGCCACCTCTCC 60
Cc 61 TCGAGGGGCAATCAGATGTTAGGAGGGGCTTATTTAGTCTGGTACAGAGAAAGCTTGG 120
Qy 61 TCGAGGGGCAATCAGATGTTAGGAGGGGCTTATTTAGTCTGGTACAGAGAAAGCTTGG 120
Db 121 CAGGCTCCAGGCTCCATCTATGTATCATCATCATCATCATCATCATCATCATCATCAT 180
Qy 121 CAGGCTCCAGGCTCCATCTATGTATCATCATCATCATCATCATCATCATCATCATCAT 180
Cc 181 TCCATGCGAGTGGGCTCTGGAGAGAGATTTCTATCTTCAATCATCATCATCATCATCAT 240
Qy 181 TCCATGCGAGTGGGCTCTGGAGAGAGATTTCTATCTTCAATCATCATCATCATCATCAT 240
Db 241 GATTTTCAGTGTACTTACTTCTGACAGATATGTTGGTCTACCGTGG---TTCGGCCAGGG 297
Qy 241 GATTTTCAGTGTACTTACTTCTGACAGATATGTTGGTCTACCGTGG---TTCGGCCAGGG 297
Db 298 ACCAAGGTGGAACTCAAA 315
Qy 301 ACCAAGTGGAGATCAAA 318

RESULT      4
ID US-08-300-386A-2 STANDARD: DNA; UNC; 646 BP.
AC XXXXX
DI 01-JAN-1990
DE Sequence 2, Application US/08300386A
CC Sequence 2, Application US/08300386A
CC Patent No. 5567948
CC GENERAL INFORMATION:
CC APPLICANT: Barbas, Carlos F.III
CC APPLICANT: Burton, Dennis R.
CC APPLICANT: Lerner, Richard A.
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT
CC CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
```

```
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10566 No 56K7e88th Torrey Pines Road, IPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/300,386A
CC FILLING DATE: 02-SEP-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILLING DATE: 28-DEC-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/826,623
CC FILLING DATE: 27-JAN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILLING DATE: 30-SEP-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILLING DATE: 02-FEB-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 646 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHEICAL: NO
CC ANTI-SENSE: NO
CC Sequence 646 BP: 162 A; 187 C; 170 G; 127 T; 0 other;

Query Match      81.4%: Score 259; DB 7; Length 646;
Best Local Similarity 93.1%: Pred.No 1.50e-172;
Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Db 1 GAGTTCACGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGAGCCACCTCTCC 60
Qy 1 GAGTTCACGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGAGCCACCTCTCC 60
Db 61 TCGAGGGGCAATCAGATGTTAGGAGGGGCTTATTTAGTCTGGTACAGAGAAAGCTTGG 120
Qy 61 TCGAGGGGCAATCAGATGTTAGGAGGGGCTTATTTAGTCTGGTACAGAGAAAGCTTGG 120
Db 121 CAGGCTCCAGGCTCCATCTATGTATCATCATCATCATCATCATCATCATCATCATCAT 180
Qy 121 CAGGCTCCAGGCTCCATCTATGTATCATCATCATCATCATCATCATCATCATCATCAT 180
Cc 181 TCCATGCGAGTGGGCTCTGGAGAGAGATTTCTATCTTCAATCATCATCATCATCATCAT 240
Qy 181 TCCATGCGAGTGGGCTCTGGAGAGAGATTTCTATCTTCAATCATCATCATCATCATCAT 240
Db 241 GATTTTCAGTGTACTTACTTCTGACAGATATGTTGGTCTACCGTGG---TTCGGCCAGGG 297
Qy 241 GATTTTCAGTGTACTTACTTCTGACAGATATGTTGGTCTACCGTGG---TTCGGCCAGGG 297
Db 298 ACCAAGGTGGAACTCAAA 315
Qy 301 ACCAAGTGGAGATCAAA 318
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RESULT 5
ID PCT-US94-01258-2 STANDARD; DNA; UNC; 646 BP
AC xxxxxx
DE 01-JAN-1900
DT Sequence 2, Application PCT/US9401258.
CC Sequence 2, Application PCT/US9401258
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC CHAINS
CC NUMBER OF SEQUENCES: 61
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01258
CC FILING DATE: 02-FEB-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/012,566
CC FILING DATE: 02-FEB-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/174,674
CC FILING DATE: 28-DEC-1993
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 646 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
SQ Sequence 646 BP; 162 A; 187 C; 170 G; 127 T; 0 other;

Query Match 81.4%; Score 259; DB 12; Length 646;
Best Local Similarity 93.1%; Pred. No. 1,50e-172;
Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1.

Db 1 GAGCTCAGGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCC 60
QY 1 GAGCTCAGGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCC 60
Db 61 TCCAGGCGCCAGTACAGTGTAGCAGGGGCTACTTAGCTGTACCCAGCAAAACCTTGGC 120
QY 61 TCCAGGCGCCAGTACAGTGTAGCAGGGGCTACTTAGCTGTACCCAGCAAAACCTTGGC 120
Db 121 CAGGCTCCAGGCTCCTCATCTATGTTAGTATCCAGGCGCCAGTGGCATCCAGACAGG 180
QY 121 CAGGCTCCAGGCTCCTCATCTATGTTAGTATCCAGGCGCCAGTGGCATCCAGACAGG 180
Db 181 TCCAGTGGCAGTGGGCTGGGAGAGACTTCACTCTCCAGCATCAGCAGACTGGAGCCGTA 240
QY 181 TCCAGTGGCAGTGGGCTGGGAGAGACTTCACTCTCCAGCATCAGCAGACTGGAGCCGTA 240
Db 241 GATTTTCAGTGTACTGTCTCAGCAGTATGGTGGCTCACCCTGG- --TTGGCCCAAGGG 297
QY 241 GATTTTCAGTGTACTGTCTCAGCAGTATGGTGGCTCACCCTGG- --TTGGCCCAAGGG 297
Db 298 ACCAAGGTGGAAGTCAAA 315
QY 301 ACCAAGTTGGAGATCAA 318

RESULT 6
ID, US-08-276-852-152 STANDARD; DNA; UNC; 729 BP.
AC xxxxxx
DE 01-JAN-1900
DT Sequence 152, Application US/08276852
CC Sequence 152, Application US/08276852

CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 200,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCPI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 152:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 729 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 9..715
SQ Sequence 729 BP; 173 A; 208 C; 192 G; 156 T; 0 other;

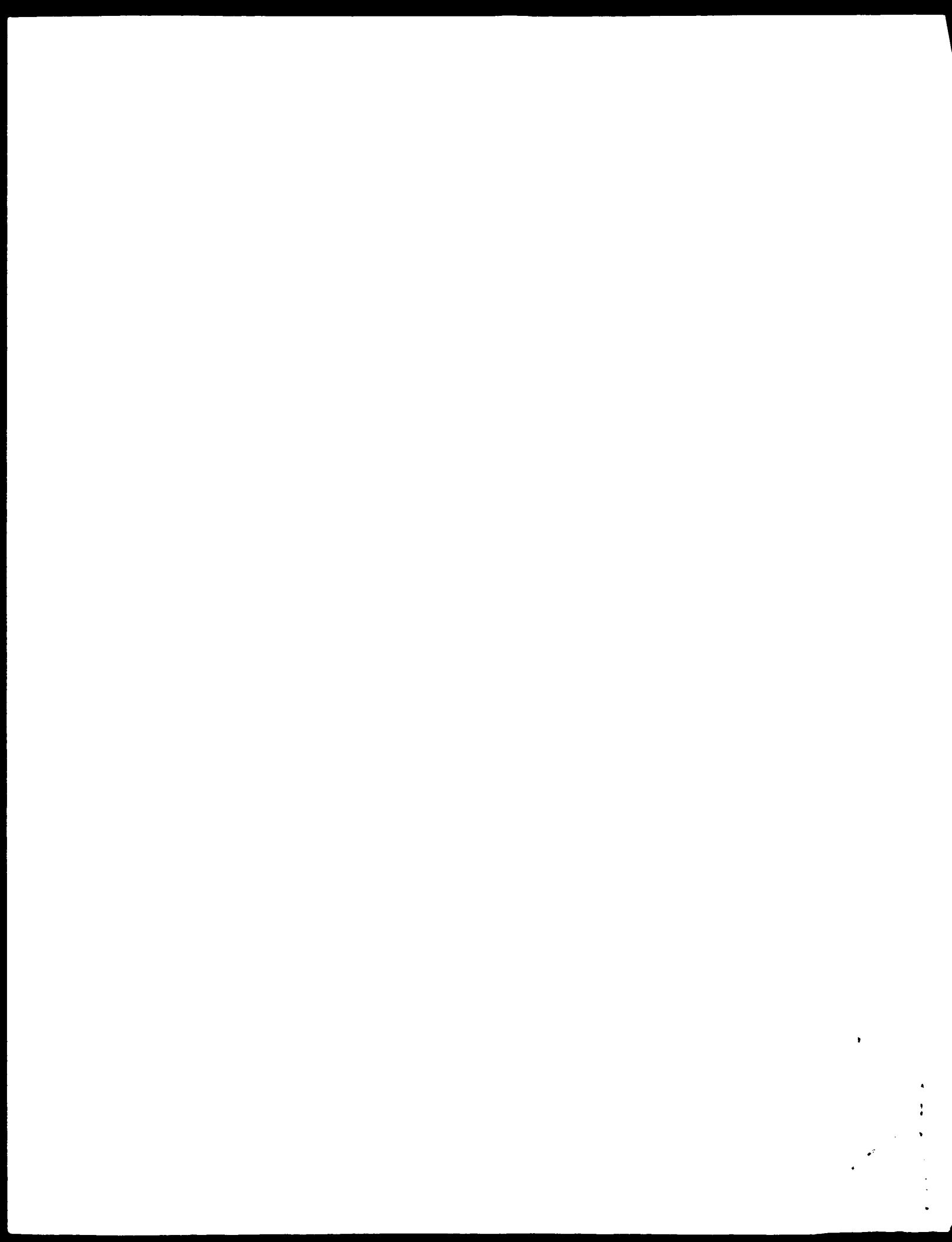
Query Match 69.5%; Score 221; DB 7; Length 729;
Best Local Similarity 85.1%; Pred. No. 7.20e-144;
Matches 268; Conservative 0; Mismatches 47; Indels 0; Gaps 0.

Db 78 CTCAGCAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCTCTGT 137
QY 4 CTCAGCAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGAGCCACCTCTCTCTGT 63
Db 138 AGGTCCAGTCCAGCAGATTCGAGCGCGCGGTAGCTTGGGTACAGTACAACTTGGGTAG 197
QY 64 GGGGCGAGTCCAGAGTGTAGGAGGCACTTACTTAGCTGTGTACAGTACAAACTTGGGTAG 123
Db 198 GCTCCAAAGGCTGATCATATGATGTTTCCAAATAGGGGCGCTCTGGCATCTCCAGACAGTTC 257
QY 124 GCTCCAGGCTCTCTCATCTATGTTGTTATCCAGGAGGCGCACTGGCATCCAGACAGTTC 193
Db 258 ACCGCGAGTGGGTCTGGGAGACAGATTCATCTCTCAAAATACAAAGTGGAGTGGAGAGAC 317
QY 184 AGTGGCAGTGGGTCTGGGAGACAGATTCATCTCTCAAAATACAAAGTGGAGTGGAGAGAI 243
Db 318 TTTGCACTGTACTACTGTCTAGTGTATGGTGGCTCTCTGCTACACTTTTGGCCAGGCGACC 377

DT 01-JAN-1997
DE Sequence 180 Application US/08053131
CC Sequence 180 Application US/08053131
CC Patent No. 5661016
CC GENERAL INFORMATION:
CC APPLICANT: Lohberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053.131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 180:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 900 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: GDS
CC LOCATION: Join(180..227, 397..693)
CC Sequence 900 bp: 225 A 244 G 254 G 257 A 0 other;
SQ
Query Match 56.7% Score 212; DB 7; Length 900;
Best Local Similarity 93.5%; Pred. No. 4.25e-137;
Matches 244; Conservative 0; Mismatches 14; Indels 3; Gaps 1;
Db 421 ACACAGTCTCCAGGACAGCTGCTTTGGTCTTACAGGGGAAAGAGACACCTCTCTCTCGCAGG 480
QY 7 ACCGAGTCTCCAGGACAGCTGCTTTGGTCTTACAGGGGAAAGAGACACCTCTCTCTCGCAGG 56
Db 481 GGCAGTCCAGGACAGCTGCTTTGGTCTTACAGGGGAAAGAGACACCTCTCTCTCGCAGGCT 537
QY 57 GGCAGTCCAGGACAGCTGCTTTGGTCTTACAGGGGAAAGAGACACCTCTCTCTCGCAGGCT 126
Db 538 GTTAGGCT 597
QY 127 CCAGAGTCT 186
Db 598 GGCAGTCCAGGACAGCTGCTTTGGTCTTACAGGGGAAAGAGACACCTCTCTCTCGCAGG 657
QY 187 GGCAGTCCAGGACAGCTGCTTTGGTCTTACAGGGGAAAGAGACACCTCTCTCTCGCAGG 246

DB 658 GCAGTCT
QY 247 GCAGTCT

Search completed: Tue Feb 24 14:09:26 1998
Job time : 60 secs.



WIRE

(TM)

Release 2.10 John F. Collins, Biocomputing Research Unit,
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Mpsrch_nnn 3 - n a database search using Smith-Waterman algorithm

Run on: Tue Feb 24 07:55:39 1998 Maspar time 48.40 seconds
758,215 Million cell updates/sec

Tabular output not generated

Title: >US-08-844-215-17
Description: (1-318) from US08844215.seq
Perfect Score: 318
N.A. sequence: 1 GAGCTGACGCGAGTGTCCAGG
Comp: CUCGATGCGGTAAGATTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57699962 bases x 2

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: n-genes30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.015; Variance 4.892; scale 1.638

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result No	Score	Query Match	Length	ID	Description	Pred. No.
1	278	87	4	Q49155	F105 rearranged varia	1,348,169
2	276	86	8	Q49155	F105V-F105V	1,348,169
3	270	84	9	Q49155	Immunoglobulin x101.2	4,628,164
4	267	84	0	Q49155	Human V-kappa gene vk	5,510,162
5	267	84	0	Q49155	DNA fragment vk101.2	5,510,162
6	267	84	0	Q49155	Human DNA fragment vk	5,510,162
7	264	83	0	Q49155	Anti-lung tumor anti	5,510,162
8	262	82	4	Q49155	Light chain of Amb 31	1,588,159
9	262	82	4	Q49155	vk105-1k2	1,588,159
10	261	82	1	Q49155	pCMB3 expression vec	7,780,158
11	251	82	1	Q49155	Expression vector, pp	7,780,158
12	250	81	4	Q49155	pCMB3 antitoxins	1,888,156
13	248	81	4	Q49155	Anti-tetanus toxoid 1	1,888,156
14	257	80	8	Q49155	Gene for IV region of	4,538,155
15	252	79	2	Q49155	vicarative cellis-as	1,200,151

16	249	78	3	Q49155	vicarative cellis-as	1,200,151
17	239	75	2	Q49155	Anti-F. dermatosa sc	1,210,142
18	239	75	2	Q49155	Anti-pseudomonas aer	1,210,142
19	229	72	0	Q49155	Sequence coding huma	9,428,136
20	224	70	4	Q49155	PM4-7 fragment, over	2,610,142
21	221	69	5	Q49155	DNA encoding modified	2,610,142
22	221	69	5	Q49155	Nucleotide sequence o	2,610,142
23	216	67	9	Q49155	DNA fragment vk55.3	9,270,127
24	216	67	9	Q49155	Human DNA fragment vk	9,270,127
25	216	67	9	Q49155	Human V-kappa gene vk	9,270,127
26	212	65	7	Q49155	DNA fragment vk55.5	4,630,124
27	212	65	7	Q49155	Human V-kappa gene vk	4,630,124
28	212	65	7	Q49155	Human DNA fragment vk	4,630,124
29	209	65	7	Q49155	IgG light chain varia	5,310,122
30	209	65	7	Q49155	IB1 IgG aberrant ligh	5,310,122
31	164	51	6	Q49155	cDNA encoding kappa 1	2,970,91
32	150	47	2	Q49155	Human immunoglobulin	9,250,82
33	150	47	2	Q49155	HIL2P Ab L chain V re	9,250,82
34	148	46	5	Q49155	Anti-pseudomonas aer	2,090,80
35	148	46	5	Q49155	Human anti-pneumococ	2,090,80
36	148	46	5	Q49155	Anti-pseudomonas aer	2,090,80
37	147	46	2	Q49155	Coding sequence for 1	9,930,80
38	146	45	9	Q49155	Human immunoglobulin	4,690,79
39	144	45	3	Q49155	cDNA contg. an ORF fo	1,050,77
40	143	45	0	Q49155	Anti-TCF beta-2 seq	4,980,77
41	141	44	3	Q49155	Coding sequence for 1	1,110,75
42	141	44	3	Q49155	Encephal V region of 1	1,110,75
43	141	44	3	Q49155	Encephal V region of 1	1,110,75
44	141	44	3	Q49155	Encephal V region of 1	1,110,75
45	140	44	0	Q49155	DNA encoding light ch	5,260,75

ALIGNMENTS

RESULT 1
ID Q49155 standard: cDNA: 387 BP.
AC Q49155:
DI 01-NOV-1993 (first entry)
DE F105 rearranged variable region light chain.
KW Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;
KW CDA; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency; ss
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 1 57
FT /*tag= a
FT mat_peptide 58...387
FT /*tag= b
PN WO931232-A.
PD 24-JUN-1993.
PF 10-DEC-1992; W10929.
PP 10-DEC-1991; US-804652.
PA (DAND) DANA FARBER CANCER INST INC.
PA (NEWB) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
DR WPI: 93-214174/26.
DP P-PSDB: P41286.
DI DNA segments encoding monoclonal antibody - which binds to gp120
PI and neutralises HIV, for treating AIDS, and for diagnosing and
PI monitoring HIV infection
ES Claim 1, Page 79, 109pp; English
CC RNA from the known hybridoma F105 was converted to cDNA and this
CC subjected to PCR amplification using primers which are appropriate
CC parts of the heavy or light chains and having restriction sites to
CC permit cloning. The extension products were isolated and sequenced.
CC The recombinant human monoclonal antibody (MAb) binds to a
CC discontinuous epitope on the HIV gp120 envelope glycoprotein. Blocks
CC the binding of gp120 to the CD4 receptor, and neutralises a broad
CC range of HIV isolates. The MAb may be used to treat immune
CC deficiency, esp at doses of 0.1-10 mg/kg.
SQ Sequence 387 bp; 88 A; 111 C; 101 G; 87 T;
Query Match 87.4%; Score 278, DB 7; Length 387;

Best Local Similarity 94.6%; Pred. No. 1.34e-169; Matches 295; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db 73 acqagctccagcagccctcttctctcaggggaaagagccaccctctcctcagc 132
 QY 7 ACCGAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 133 gccadtcagagtggttagcagcaggtacttgccttggtaccagcagaaacctggccagct 192
 QY 67 GCCAGTCCAGAGTGTAGGAGCAACTACTTAGCTGCTGCTAGCAGCAAAACCTGGCCAGGCT 126

Db 193 cccagctcctcatatggtgcacacagcagggccactggccatccacagcaggttcagt 252
 QY 127 CCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 193 cccagctcctcatatggtgcacacagcagggccactggccatccacagcaggttcagt 252
 QY 127 CCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 253 gccagtggtgtcggcagcagcttactctcaccatcagcagagtgaggcctgaagatttt 312
 QY 187 GCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 313 gccagtggtgtcggcagcagcttactctcaccatcagcagagtgaggcctgaagatttt 312
 QY 187 GCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 373 ctggagagatcaaa 384
 QY 307 TTGGAGATCAAA 318

RESULT 2
 ID Q42707 standard; DNA; 390 BP.
 AC Q42707;
 DT 01-NOV-1993 (first entry)
 DE F105VK-F105JK.
 KW Monoclonal antibody; MAbs; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
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 FT /*tag= a
 FT mat_protein 61 390
 FT /*tag= b
 FT misc_RNA 1..351
 FT /*tag= c
 FT label= F105VK 352..390
 FT misc_PNA
 FT /*tag= d
 FT label= F105JK 130 165
 FT misc_PNA
 FT /*tag= e
 FT label= CDR1 211..231
 FT misc_PNA
 FT /*tag= f
 FT label= CDR2 328..354
 FT misc_PNA
 FT /*tag= g
 FT label= CDR3
 PN W09312232-A.
 PD 24-JUN-1993
 PE 10-DEC-1992; 010928
 PR 10-DEC-1991; US-804652
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 PR Haseltine WA, Marasco WA, Posner MP, Sodroski TG;
 DR WPI: 93-214174/26.
 DP P-PSDB: R38672.
 PI DNA segments encoding monoclonal antibody - which binds to gp120
 PI and neutralises HIV, for treating AIDS, and for diagnosing and
 PI monitoring HIV infection
 PS Disclosure, Page 73-74; 10pp; English
 CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from
 CC other F105 VK sequences given elsewhere in the specification) was
 CC compared with germline gene HumvK325 (Q42706), showing 97.7%

CC similarity. By nucleotide sequence analysis, F105 appears to
 CC be derived from a member of the V κ III subgroup gene family.
 SQ Sequence 390 BP, 86 A, 115 C, 102 G, 87 T,
 Query Match 86.8%; Score 276; DB 7; Length 390;
 Best Local Similarity 96.2%; Pred. No. 3.24e-168;
 Matches 303; Conservative 0; Mismatches 9; Indels 3; Gaps 2;

Db 73 acqagctccagcagccctcttctctcaggggaaagagccaccctctcctcagc 132
 QY 7 ACCGAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 133 gccadtcagagtggttagcagcaggtacttgccttggtaccagcagaaacctggccagct 192
 QY 67 GCCAGTCCAGAGTGTAGGAGCAACTACTTAGCTGCTGCTAGCAGCAAAACCTGGCCAGGCT 126

Db 193 cccagctcctcatatggtgcacacagcagggccactggccatccacagcaggttcagt 252
 QY 127 CCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 253 gccagtggtgtcggcagcagcttactctcaccatcagcagagtgaggcctgaagatttt 312
 QY 187 GCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 313 gccagtggtgtcggcagcagcttactctcaccatcagcagagtgaggcctgaagatttt 312
 QY 187 GCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 373 aagctggagatcaaa 387
 QY 304 AAGTTGGAGATCAAA 318

RESULT 3
 ID T79922 standard; DNA; 372 BP.
 AC T79922;
 DT 09-OCT-1997 (first entry)
 DE Immunoglobulin r101-2 light chain variable region coding sequence.
 KW Immunoglobulin; variable region; heavy chain; thyrotropin receptor;
 KW thyroid stimulating activity; light chain; Basedow's disease; antibody;
 KW peripheral blood lymphocyte; ss
 OS Homo sapiens.
 PN J09140386-A.
 PD 03-JUN-1997.
 PE 22-NOV-1995; 328235.
 PE 22-NOV-1995; JP-328235.
 PA (EIKE) EIKEN KAGAKU KK.
 DR WPI: 97-344899/32.
 DR P-PSDB: W24539.
 PT Antibody containing immunoglobulin heavy chain mutation - with
 PT thyroid function stimulating activity
 PS Claim 4; Page 12; 18pp; Japanese.
 CC T79919-T79922 represent the immunoglobulin heavy and light chain variable
 CC regions isolated from peripheral blood lymphocyte strains. These
 CC sequences were isolated from the B67 and 101-2 strains of peripheral
 CC blood lymphocytes of a Basedow's disease patient. These sequences are
 CC replaced, deleted or inserted into an antibody, to create the antibodies
 CC of the invention. The antibodies of the invention have thyroid function
 CC stimulating activity, and act by combining with thyrotropin receptor. The
 CC antibody can be used in a method to detect autoantibodies which have
 CC thyroid function stimulating activity.
 SQ Sequence 372 BP; 81 A; 115 C; 95 G; 81 T;
 Query Match 84.9%; Score 270; DB 32; Length 372;
 Best Local Similarity 95.0%; Pred. No. 4.62e-164;
 Matches 285; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 73 acqagctccagcagccctcttctctcaggggaaagagccaccctctcctcagc 132
 QY 7 ACCGAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 133 gccadtcagagtggttagcagcaggtacttgccttggtaccagcagaaacctggccagct 192
 QY 67 GCCAGTCCAGAGTGTAGGAGCAACTACTTAGCTGCTGCTAGCAGCAAAACCTGGCCAGGCT 126

Db 193 cccagctcctcatatggtgcacacagcagggccactggccatccacagcaggttcagt 252
 QY 127 CCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 253 gccagtggtgtcggcagcagcttactctcaccatcagcagagtgaggcctgaagatttt 312
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Db 313 gccagtggtgtcggcagcagcttactctcaccatcagcagagtgaggcctgaagatttt 312
 QY 187 GCCAGTCTCCAGGACCCCTGCTCTGCTCCAGGGAAAGAGCCACCTCTCTGCGGG 66

Db 373 aagctggagatcaaa 387
 QY 304 AAGTTGGAGATCAAA 318

[illegible]

Query: Match

Qy	7	AGCAGTCTCCAGCAGCCCTGTTTCTTCTCAGAGGAAACAGGTCCTCTTCTGAGG	66
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Qy	67	GCCAGTCAGAGTGTATAGAGCAACTACTTAGCTCTGCTATCCAGCAAAAACCTTGCCAGGCT	126
Db	193	ccacagccctccctcctctgctggttctatccacacagaggtctgtgacacacagagacagat	252
Qy	127	CCCAAGCTCTTCATCTATCTATCTATATACAGAGGCAATGCTATATATATATATATATAT	186


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Best Local Similarity 93.4%; Pred. No. 7,78e-158;
Matches 297; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

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QY 1 GAGTTCAGAGTCACAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 50

Db 4667 tccagggcagctcagcagcttaccagccctacttagcttagcttagccagcagaacatggc 4726
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QY 61 TCCAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 126

Db 4727 cagggctccagggctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 4786
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QY 121 CAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAG 180

Db 4787 tccagggcagctcagcagcttaccagccctacttagcttagcttagccagcagaacatggc 4846
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QY 181 TCCAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 240

Db 4847 gatttgcagctcagcagcttaccagccctacttagcttagcttagccagcagaacatggc 4903
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QY 241 GATTTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAG 300

RESULT 12
ID T15203 standard; cDNA: 646 BP.
AC T15203;
DE 23-OCT-1996 (first entry)
DE PC3AP33 anti-tetanus toxoid Ig light chain variable domain cDNA
DE Mutagenesis: Ig; immunoglobulin FP framework region; variable; CDR.
KW Complementarity determining region; light; heavy chain; PCR;
KW polymerase chain reaction; antibody library; diversity; affinity;
KW immunospecificity; ss.
OS Synthetic.
PN WO9607754-A1.
PD 14-MAR-1996.
PF 01-SEP-1995; U11235.
PF 02-SEP-1994; US-6004966.
PI (SCR1 ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA.
PI WPI: 96-171625/17
DR Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
DR gene CDR - useful for prodn. of Ig heavy and light chain
PT Combinatorial antibody libraries
PS Example 1; Page 84; 125pp; English.
CC T15203 and T15203 are the heavy and light chain variable domains of
CC a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a Pcomb3
CC based expression vector. The heavy and light chain variable domains
CC are used in an example to demonstrate the prodn. of antibodies for
CC an antibody library using mutagenesis primers. Mutagenic primers of the
CC invention have sequences at their 3' and 5' ends both capable of
CC binding different framework regions linked by a sequence 6 to 50
CC nucleotides long. Different immunoglobulins produced using the
CC primers may be used to produce antibody libraries having diverse and
CC novel immunospecificities and affinities. By using mutagenic ONS an
CC extremely large population of different randomised binding sites can
CC be created and use of the universal light chain increases the number
CC of combinations which yield functional heterodimeric antibodies.
SQ Sequence 646 BP; 152 A; 187 G; 170 G; 127 T;

Query Match 91.4%; Score 259; DB 22; Length 646;
Best Local Similarity 93.1%; Pred. No. 1.88e-156;
Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Db 1 gaactcacagatcccaagaccctgtcttctgctcagggggaagagccacactctcc 60
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QY 1 GAGTTCAGAGTCACAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 60

Db 61 tccagggcagctcagcagcttaccagccctacttagcttagcttagccagcagaacatggc 120
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QY 61 TCCAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 120

Db 61 tccagggcagctcagcagcttaccagccctacttagcttagcttagccagcagaacatggc 180
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QY 61 TCCAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 180

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|||||
QY 61 TCCAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 120

Db 121 cagggctccagggctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 180
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QY 121 CAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAG 180

Db 181 tccagggcagctcagcagcttaccagccctacttagcttagcttagccagcagaacatggc 240
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QY 181 TCCAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 240

Db 241 gatttgcagctcagcagcttaccagccctacttagcttagcttagccagcagaacatggc 300
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QY 241 GATTTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAG 300

Db 298 accaaggtggaactcaaa 315
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QY 301 ACCAAGTGGAGATCAAA 318

RESULT 13
ID Q70487 standard; cDNA: 646 BP.
AC Q70487;
DE 04-APR-1995 (first entry)
DE Anti-tetanus toxoid light chain cDNA from vector, pc3AP33.
DE Polymerase chain reaction; primer: mutagenesis; PCR; amplify;
KW diversity; antibody; complementarity determining region; CDR;
KW framework; constant; light; heavy; phase; immunoglobulin; library; ss.
OS Synthetic.
PN WO9418219-A.
PD 18-AUG-1994.
PF 02-FEB-1994; U01234.
PF 02-FEB-1993; US-012566.
PF 28-DEC-1993; US-174674.
PI (SCR1 ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA.
PI WPI: 94-279673/34.
DR Oligo-nucleotides - used as PCR primers for producing increased
DR diversity antibody libraries, for screening antigens
PT Claim 21; Page 84-85; 120pp; English.
PS This sequence represents the light chain coding sequence derived from
PS the surface display phagemid expression vector, pc3AP33. pc3AP33
PS contains the bacteriophage gene III and heavy and light chain variable
PS domain sequences for encoding human Fab antibodies against tetanus toxin.
PS This sequence was pref used in the method of the invention for the
PS production of antibody libraries containing increased diversity. The
PS sequences given in Q70480-86 are primers which were used for induction
PS mutagenesis in a complementary determining region (CDR) of an
PS immunoglobulin light chain gene. These primers contain a 3' terminus
PS capable of hybridising to a first framework region, a 5' terminus
PS capable of hybridising to a second framework region and a nucleotide
PS sequence between the 5' and 3' termini having the formula (NNK)n,
PS where n is 3-24. These primers may be used to produce antibody
PS libraries with increased antibody diversity by inducing mutagenesis
PS within the CDR regions of immunoglobulin heavy or light chains that
PS are displayed on the surface of filamentous phage particles comprising
PS the library. These primers pref. mutate the light chain CDR3.
SQ Sequence 646 BP; 162 A; 187 G; 170 G; 127 T;

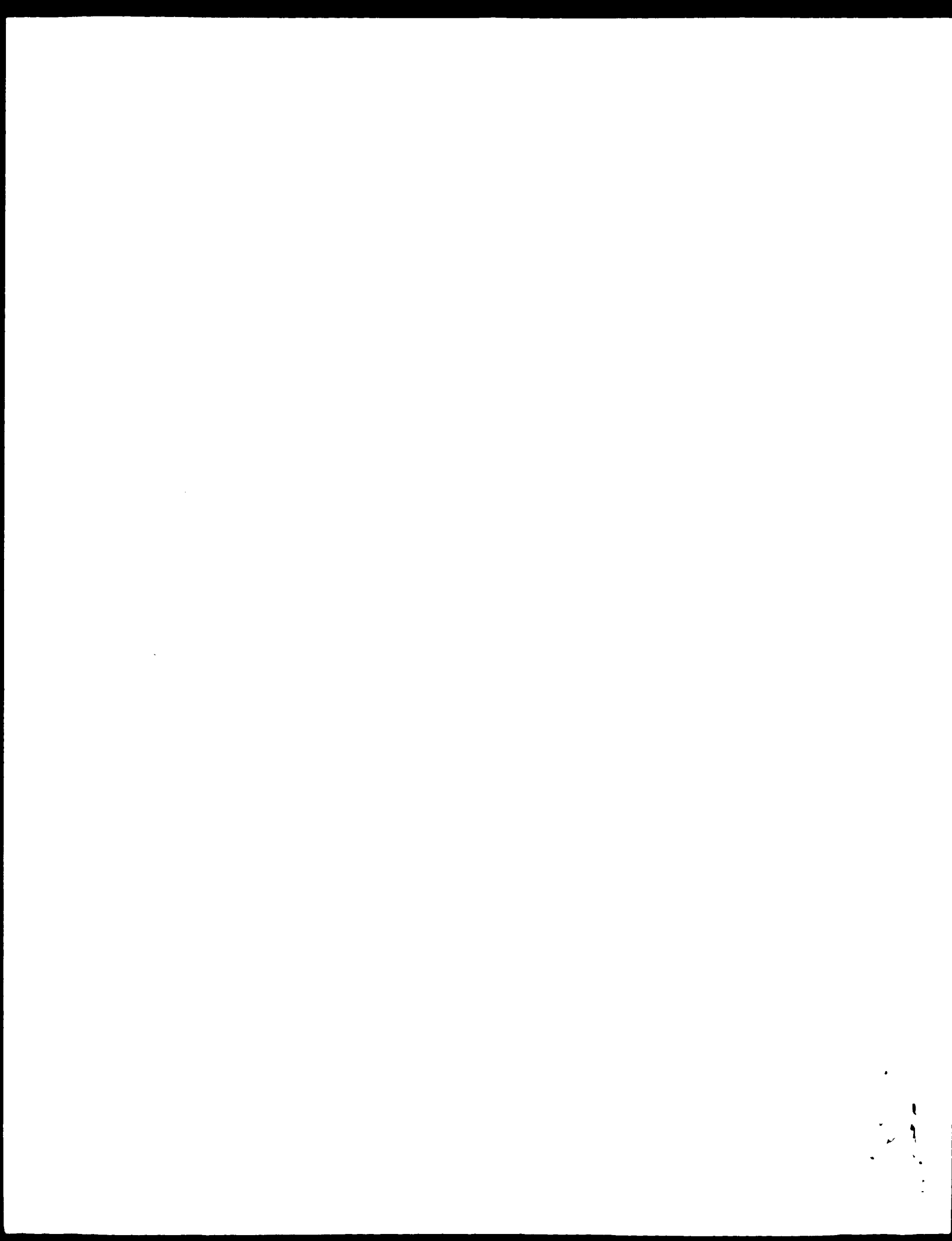
Query Match 81.4%; Score 259; DB 12; Length 646;
Best Local Similarity 93.1%; Pred. No. 1.88e-156;
Matches 296; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Db 1 gaactcacagatcccaagaccctgtcttctgctcagggggaagagccacactctcc 60
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QY 1 GAGTTCAGAGTCACAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 60

Db 61 tccagggcagctcagcagcttaccagccctacttagcttagcttagccagcagaacatggc 120
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QY 61 TCCAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAG 120

Db 121 cagggctccagggctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 180
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QY 121 CAGGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAGTCAGAG 180

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	DB	ID	Description	Pred. No.
1	284	92	5	387	90	HSBUD451	H sapiens mRNA for an	3
2	282	91	8	420	90	HSMIDKAP	human Ig rearranged k	3
3	282	91	8	330	93	HSL1P6V	H sapiens immunoglob	2
4	280	91	2	320	90	HSMICKAQ	Human Ig rearranged k	2
5	280	91	2	324	91	HSIGVITTD	H sapiens mRNA for Ig	1
6	280	91	2	324	91	HSIGVKS33	H sapiens mRNA for Ig	1
7	280	91	2	447	99	HSMIGHHA	Human Ig rearranged k	1
8	280	90	9	402	91	HS7GVIC	Human rRNA for 13S	1
9	288	90	6	320	99	HSMIKRAT	Human Ig rearranged k	1
10	288	90	6	324	95	HSU76682	Human rearranged IGM	1
11	288	90	6	402	91	HS7GVIC	Human Ig active kappa	1
12	288	90	6	402	91	HS7GVIC	Human rRNA for 13S	1
13	287	90	3	324	99	HSM1KCVG	Human sapiens Ig kappa	2
14	286	89	9	324	99	HSM1L12A	Human sapiens immunog	2
15	286	89	3	325	99	HSMMA855	Human immunoglobulin	2
16	286	89	9	364	99	HSMIGL3AC	Human Ig rearranged k	2
17	284	89	3	300	94	HSMIKCCO	Human sapiens (clone L	1
18	284	89	3	318	99	HSMIKGVY2	Human anti-papetein m	1
19	284	89	3	329	91	HS1GRHE19	H sapiens (PMP16K) m	1
20	283	89	0	312	91	HS1GRHE18	H sapiens (PMP13K) m	1
21	283	89	0	316	91	HS1GRHE20	H sapiens (PMP12K) m	1
22	282	88	7	323	99	HSMIKKAP	Human Ig rearranged k	2
23	282	88	7	390	99	HSM1GHHY	Human Ig rearranged k	2
24	280	88	1	300	99	HSMIKCOP	Human Ig rearranged k	2
25	280	88	1	343	99	HSMIKC3OM	Human Ig rearranged k	2
26	278	87	4	300	99	HSMIKC3OM	Human Ig rearranged k	2
27	278	87	4	324	94	HS034423	Human Clone 354-1A k	1
28	278	87	4	327	94	HS214567	H sapiens mRNA for im	1
29	278	87	4	327	94	HS214567	Human immunoglobulin	1
30	278	87	4	330	98	HMPABFGLJ	Human Fab fragment bi	1
31	278	87	4	330	98	HMPABFGLB	Human Fab fragment bi	1
32	278	87	4	387	97	HSM1G14L	Human sapiens Ig rearr	1
33	278	87	4	387	97	HSMANT1GPA	Human anti-glycoprote	1
34	278	87	4	429	91	HS1GR784	H sapiens rearranged	1
35	277	87	1	333	95	HSMHFRFAL	Human hepatitis B sur	1
36	277	87	1	333	95	HS024772	Human anti-HIV-1 gp12	1
37	276	86	8	300	94	HSM1KCBG	Human sapiens (clone S	1
38	276	86	8	324	94	HS034482	Human Clone 354-1A k	1
39	276	86	8	326	99	HSM1GLRM	Human sapiens (P347L)	1
40	276	86	8	326	99	HSM1GLR2	Human sapiens (P347L)	1
41	276	86	8	327	100	SC61031	Ig V kappa 1122 (Homo	1
42	276	86	8	327	99	HSMHFRFASG	Human Fab fragment bi	1
43	276	86	8	327	99	HSMHFRFASG	Human hepatitis B sur	1
44	276	86	8	333	91	HS1GR2851	H sapiens rearranged k	1
45	276	86	8	333	99	HSMIKKAA	Human anti-sialosylate	1

ALIGNMENTS

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DEFINITION	H sapiens mRNA for anti- β 2-microglobulin VL chain (V kappa 307, kappa 2).
ACCESSION	Z46345
NID	9560843
KEYWORDS	anti- β 2-microglobulin kappa chain, anti- β 2-microglobulin light chain; joining region; variable region.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 387)
AUTHORS	Mamoudi M., Edwards J., Cairns, E. and Bell D.
TITLE	Molecular characterization of natural human anti- β 2-microglobulin antibodies
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 387)
AUTHORS	Mamoudi M.

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*****
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(TM)

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MPSrch_nu n.a - n.a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:45:59 1998: MasPar time 407.74 Seconds
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Perfect Score: 318
M.A. Sequence: 1 GAGTCACCGACGCTGTCCAGC GCATCAAGTTCGATGAATAAA
Comp: CTTGAGTGGTGTAAGAGTAGC TTTGATGATGATCAATGATTAATT

Scoring table: TABLE default
Gap 5

Match STD : Dbase 0: Query 0

Searched: 43061 seqs, 71021776 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

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9:HUM2 10:HM3 11:INV 12:INV2 13:OPN 14:MAM 15:VPT
16:PLN 17:PPO1 18:PPO2 19:POC 20:SYN 21:UNA 22:VIP
genbank101
23:BCR1 24:RC12 25:RC13 26:RC14 27:RC15 28:RC16 29:RC17
30:RC18 31:RC19 32:RC110 33:RC111 34:RC112 35:RC113
36:GEN1 37:GEN2 38:GEN3 39:GEN4 40:GEN5 41:GEN6 42:HTG1
43:HTG2 44:HTG3 45:HTG4 46:HTG5 47:INV 48:INV2 49:INV3
50:INV4 51:INV5 52:INV6 53:INV7 54:INV8 55:INV9 56:INV10
57:INV11 58:INV12 59:MAM1 60:MAM2 61:MAM3 62:VPT1
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70:PAT5 71:PAT6 72:PAT7 73:PHG 74:PM1 75:PLN2 76:PLN3
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96:PR11 97:PR12 98:PR13 99:PR14 100:PR15 101:PR116
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142:part1 143:part2

Statistics: Mean = 0.77 Variance = 5.24 Scale = 2.197

Pred No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being plotted.

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TITLE Direct Submission
 JOURNAL Submitted (24-OCT-1994) Mahmudi M., University of Western Ontario,
 Medicine and Microbiology and Immunology, University Hospital Room
 BRE-12, London, Ontario, Canada, N6A 5A5

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little or no somatic hypermutation
 J. Immunol 143 (2): 65d-7n5 (1989)
 MEDLINE 89292697
 COMMENT Draft entry and printed sequence for [1] kindly submitted by
 L F Pratt, 20-SEP-1989

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Db 307 gtggagatcaaa 318
 QY 307 TTGGAGATCAAA 318

RESULT 3
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 DEFINITION H.sapiens immunoglobulin kappa chain V-J region (s17b VL).
 ACCESSION 246310
 NID 9601982
 KEYWORDS Immunoglobulin; kappa chain: V-J region.
 SOURCE Human.
 ORGANISM Homo sapiens
 Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 330)
 AUTHORS Chapman,C.J., Spellerberg,M.B., Hamblin,J. and Stevenson,F.K.
 TITLE Pattern of usage of the VH4-21 gene by B lymphocytes in a patient
 with EBV infection indicates ongoing mutation and class switching
 JOURNAL Mol. Immunol. 32 (5): 347-353 (1995)
 MEDLINE 95257976
 REFERENCE 2 (bases 1 to 330)
 AUTHORS Chapman,C.J.

TITLE Direct Submission
JOURNAL Submitted (20-OCT-1994) Caroline J Chapman, Molecular Immunology Group, Tenovus Research Laboratory, Southampton University Hospitals, Tremona Road, Southampton, SO16 6YD, United Kingdom
FEATURES Location/Qualifiers
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 QY 307 TTGGAGATCAAA 318
RESULT 4 HUMICKAQ 320 bp PNA PPI 04-JAN-1995
DEFINITION Human Ig rearranged kappa chain V-J1-region gene, partial cds.
ACCESSION M28156
NID g185906
KEYWORDS C-region; J-region; V-region; immunoglobulin light chain; immunoglobulin-kappa; Human lymphocyte DNA, from patient KB5 with small lymphocytic lymphoma.
SOURCE Homo sapiens
ORGANISM Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 320)
AUTHORS Pratt, L.F., Passentini, L., Larrick, J., Robbins, B., Banks, P. M. and Kipp, J.J.
TITLE Ig V region gene expression in small lymphocytic lymphoma with little or no somatic hypermutation
JOURNAL J. Immunol. 143 (2): 669-705 (1989)
ENTRY 89262697
COMMENT Draft entry and printed sequence for [1] kindly submitted by L.F. Pratt, 20-SEP-1989
FEATURES Location/Qualifiers
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TITLE Direct Submission
JOURNAL Submitted (20-OCT-1994) Caroline J Chapman, Molecular Immunology Group, Tenovus Research Laboratory, Southampton University Hospitals, Tremona Road, Southampton, SO16 6YD, United Kingdom
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 Db 307 atggaatacaaa 318
 QY 307 TTGGAGATCAAA 318
RESULT 5 HSICVLTD 324 bp PNA PPI 06-SEP-1997
LOCUS H.sapiens mRNA for Ig light chain anti-TTid, variable region.
DEFINITION Y04594
ACCESSION Y04594
NID g1834498
KEYWORDS anti-TTid gene; immunoglobulin variable region light chain.
SOURCE human
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 324)
AUTHORS Weisschof, M., Terness, P., Schoeneberg, A., Kiprianov, S., Land, A., Kleist, C., Vogt, A., Pfeiffer, K., Little, M. and Weissmayer, D.
TITLE Isolation and characterization of a human anti-TTid scfv antibody and its bivalent derivative
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 324)
AUTHORS Weisschof, M.
TITLE Direct Submission
JOURNAL Submitted (02-OCT-1996) M. Weisschof, Universitaet Heidelberg, Institute of Immunology, Department of Transplantation Immunology, INF 305, 69120 Heidelberg, FRG
COMMENT Related sequence: L28046.
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Best Local Similarity 96.5%; Pred. No. 1.63e-232;
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Qy 247 GCAGTGTATTACTGTCCAGCAGTATGTAGTCTACCTCGGACTTTTGGCCAGGGGACCAAG 306
Db 313 gtggagatcaaaa 324
Qy 307 TTGGAGATCAAA 318
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LOCUS H5IGVK303 324 bp PNA PPI 30-MAP-1995
DEFINITION H.sapiens mRNA for Ig kappa light chain variable region
(V-J), subgroup III (clone C3).
ACCESSION X73863
NID 9516187
KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup III;
Ig variable region; immunoglobulin.
SOURCE Homo sapiens
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 324)
AUTHORS Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B.,
Colls, J.C., Pegg, C.A.S., Rees-Smith, B., and Burton, D.R.
TITLE Probing the human anti-thyroid peroxidase repertoire of a
Hashimoto's thyroiditis patient using combinatorial phage display
libraries
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 324)
AUTHORS Hexham, J.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of
Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western
Bank, Sheffield S10 2UH, UK
REFERENCE 3 (bases 1 to 324)
AUTHORS Hexham, J.M., Furmaniak, J., Pegg, C., Burton, D.R. and Smith, R.P.
TITLE Cloning of a human autoimmune response preparation and sequencing
of a human anti-thyroglobulin autoantibody using a combinatorial
approach

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Autoimmunity 12 (2), 135-141 (1992)
JOURNAL 92314301
MEDLINE
REFERENCE 4 (bases 1 to 324)
AUTHORS Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B.,
Colls, J.C., Pegg, C., Rees-Smith, B. and Burton, D.R.
TITLE Cloning and characterisation of 170 autoantibodies using
combinatorial phage display libraries
JOURNAL Autoimmunity 17 (3), 167-179 (1994)
MEDLINE 95035699
FEATURES
Location/Qualifiers
1..324
/organism="Homo sapiens"
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Best Local Similarity 95.6%; Pred. No. 1.63e-232;
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Qy 121 CAGGCTCCCAAGGCTCTCTATCTATGTGTATGATCCAGAGAGGCGCATCGATCCAGACAG 180
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Qy 301 ACCAAGTTGGAGATCAAA 318
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LOCUS HUMIGHHA 447 bp mRNA PPI 04-NUV-1994
DEFINITION Human Ig rearranged gamma-chain MPNA V-region, partial cds.
ACCESSION L03162
NID g185397
KEYWORDS V-region; immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Homo sapiens (tissue library: BMHIV) adult bone marrow cDNA to
mRNA.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS Collier, I.A., Cohen, P., O'Kennedy, P., Barbas, C.F. III, Burton, D.R.
and Lerner, R.A.
TITLE A binary plasmid system for shuffling combinatorial antibody
libraries
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10076-10080 (1992)
MEDLINE 93066172
FEATURES Location/Qualifiers

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REFERENCE 1 (bases 1 to 320)
AUTHORS Pratt, I. F., Passentini, J., Larrick, J., Robbins, B., Banks, P. M. and
        Kipps, T. J.
TITLE Ig V region gene expression in small lymphocytic lymphoma with
        little or no somatic hypermutation
JOURNAL J. Immunol. 143 (2): 699-705 (1989)
MEDLINE 89092597
COMMENT Draft entry and printed sequence for [1] kindly submitted by
        L.F. Pratt, 20-Sep-1989.
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Qy 307 TTGGAGATCAAA 318
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LOCUS Human rearranged IgM light chain V region mpna, partial cds
DEFINITION
ACCESSION U76682
NID q1673602
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
        Vertebrata; Euthera; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 324)
TITLE Ig V region gene usage by autoreactive MoAbs
JOURNAL Unpublished

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REFERENCE 2 (bases 1 to 324)
AUTHORS Aguilera, I.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1996) Aguilera I. Hospital U Virgen del Rocío,
        Immunology, Manuel Siurot s/n, Seville, Spain, 41013
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Best Local Similarity 96.2%; Pred. No. 1.14e-230;
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Dn 13 acagctctccagcagccctgtctgtctccaggggaagagccacctctctcagcgg 72
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Qy 307 TTGGAGATCAAA 318
RESULT 11 HUMICKAI 402 bp mpna PFI 15-DEC-1989
LOCUS Human Ig active kappa chain mpna V-region (V-11-7) clone NOV.
DEFINITION
ACCESSION M27025
NID g185845
KEYWORDS C-region; V-region; immunoglobulin light chain;
        immunoglobulin-kappa; processed gene.
SOURCE Human salivary gland B lymphocyte cDNA to mpna, clone NOV.
ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
        Vertebrata; Euthera; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 402)
TITLE Molecular characterization of a major autoantibody-associated
        cross-reactive idiotype in Sjogren's syndrome
JOURNAL J. Immunol. 142, 4261-4268 (1989)
MEDLINE 89256674
COMMENT Draft entry and printed copy of sequence kindly submitted by
        T.J. Kipps, 16-AUG-1989.
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DEFINITION Homo sapiens immunoglobulin light chain (HLH114) mRNA, V-region.
ACCESSION L43118
NID g871819
KEYWORDS digoxin-specific immunoglobulin M; light chain; light chain
SOURCE variable region of HLH114; variable region.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo
REFERENCE 1 (bases 1 to 324)
AUTHORS Danielsson,L., Furbering,C., Ohlin,M., Hultman,L., Abrahamson,M.,
Carlsson,P. and Forrebaeck,C.A.
TITLE Human monoclonal antibodies with different fine specificity for
digoxin derivatives: cloning of heavy and light chain variable
region sequences
JOURNAL Immunology 74 (1), 50-54 (1991)
MEDLINE 92039780

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FEATURES
source Location/Qualifiers
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Matches 299; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 13 acgcaagtccagcagccctgtcttctccaggggaaagaccacccctctctgcagg 72
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QY 307 TTGGAGATCAAA 318

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LOCUS HUMMAB55 325 bp mRNA PRI 09-APR-1997
DEFINITION Human immunoglobulin (mAb55) light chain V region mRNA, partial
sequence.
ACCESSION D84139
NID g1255609
KEYWORDS immunoglobulin light chain V region.
SOURCE Homo sapiens B cell hybridoma cell_line:mab55 producing hybridoma
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ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 325)
AUTHORS Ikematsu,H.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1996) to the EMBL/EMBL/GenBank databases.
Hideoyuki Ikematsu, Kyushu University, Department of General
Medicine; 3-1-1 Maidashi, Higashi-ku, Fukuoka, Fukuoka 812, JAPAN
(E-mail:ikematsu@po.riijnet.or.jp, Tel:092-641-1151,
Fax:092-691-7974)
2 (bases 1 to 322)
AUTHORS Ikematsu,H.
TITLE Light chain V region sequence
JOURNAL Unpublished (1996)
FEATURES Location/Qualifiers
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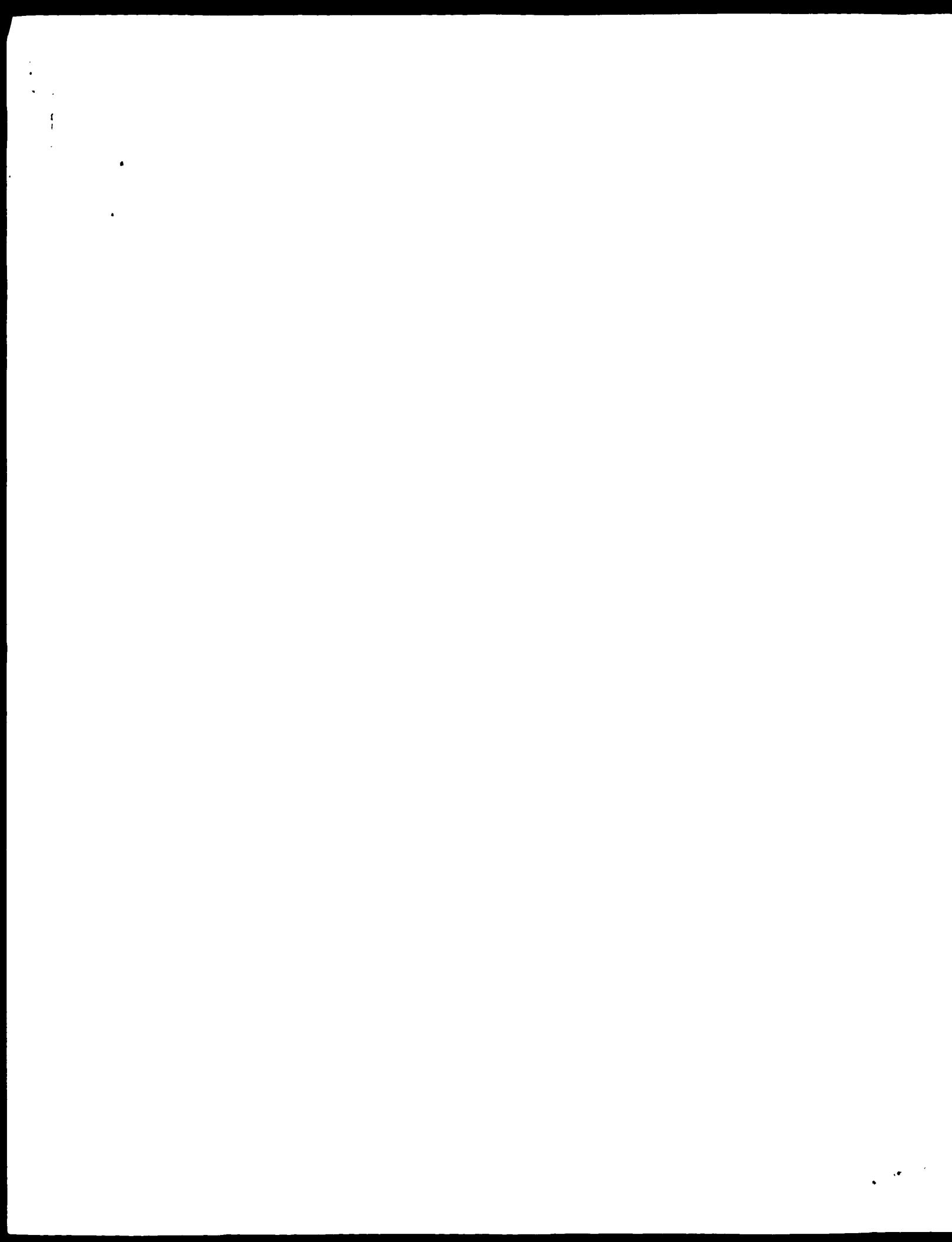
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/product="immunoglobulin light chain V-J region"
/db_xref="PID:d1020337"
/db_xref="PID:q1944486"
/translation="EIVLISPSJLSPSPATLSLHANQSVSSSYLAWYLKPSQA
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TKVEIK"

BASE COUNT 76 a 91 c 90 g 68 t
ORIGIN

Query Match 89.9% Score 286 DB 99 Length 325
Best Local Similarity 95.8% Pred. No. 8,00e-229
Matches 299: Conservative 0 Mismatches 13 Indels 0 Gaps 0

```
DB 13 aacgaagctccagagacccctgtctgtctcagagagaaagaccctctcctcag 72
   |||||||
QY 7 AGGCAAGCTCTAAGAACCTTCTTTCTCTCAAGSAAAGAACCTCTCTGCGG 66
   |||||||
DB 73 gccagtcagatgtttacagcagcagctacttagcctgtgtaccagcaaaacctgaccagct 132
   |||||||
QY 67 GCCAGTCAGATGTTAGSAGCAACTTACGCTGTGTACGACAAACCAACCTGCGCAGGCT 126
   |||||||
DB 133 cccagagctccatcctataggtgcatccagcagagccactgcatccagacaggttcagt 192
   |||||||
QY 127 CCAAGCTCTCTATCTATGCTATGTAATAGSAGCACTGATGCAAGAACAGSITCACT 186
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DB 193 ggcagtgatctgagacagacttcaactcaccatccagcagcagcctgagcctgaagatctt 252
   |||||||
QY 187 GGTATGATGCTTGGACACAACTTTCATCTTCACATACAGCACTGAGACCTGAGGATTTT 246
   |||||||
DB 253 gcaagtattacttcaagcagatattgttagctaccgagagacgttcggccaaagagccaaag 312
   |||||||
QY 247 GCAGTGATATACCTGACAGATATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 306
   |||||||
DB 313 atggaatcaaa 324
   |||||
QY 307 TTGAGATCAAA 318
```

Search completed: Tue Feb 24 07:55:19 1998
Job time : 560 secs.



WATERMAN

Release 2.1D John F. Collins, Biocomputing Research Unit,
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MPSrch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:42:43 1998. MaxFai: time 110.86 seconds
Tabular output not generated.

Title: >US-08-844-215-16
Description: (1-312) from US08844215.seq
Percent Score: 312
N.A. Sequence: 312 1 GAGCTCAGTCACTGCTCTCTAGC
Comp. CTTGAGTACAGTACAGAGAGTCTG

Scoring table: TABLE default
Gap 5
Nmatch STD. Dkase 0. Query 0
Searched: 33433 seqs, 126143548 bases x 2
Post-processing: Minimum Match 04
Listing first 45 summaries

Database: STS
9:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8
9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19 20:STS20
21:STS21 22:STS22 23:STS23 24:STS24 25:STS25 26:STS26
27:STS27 28:STS28 29:STS29 30:STS30 31:STS31 32:STS32
33:STS33 34:STS34 35:STS35 36:STS36 37:STS37 38:STS38 39:STS39
40:STS40 41:STS41 42:STS42 43:STS43 44:STS44 45:STS45
46:STS46 47:STS47 48:STS48 49:STS49 50:STS50 51:STS51
52:STS52 53:STS53 54:STS54 55:STS55 56:STS56 57:STS57 58:STS58
59:STS59 60:STS60 61:STS61 62:STS62 63:STS63 64:STS64
65:STS65 66:STS66 67:STS67 68:STS68 69:STS69 70:STS70
71:STS71 72:STS72 73:STS73 74:STS74 75:STS75 76:STS76
77:STS77 78:STS78 79:STS79 80:STS80 81:STS81 82:STS82
83:STS83 84:STS84 85:STS85 86:STS86 87:STS87 88:STS88
89:STS89 90:STS90 91:STS91 92:STS92 93:STS93 94:STS94
95:STS95 96:STS96 97:STS97 98:STS98 99:STS99 100:STS100

Statistics: Mean 9.886; Variance 1.971; scale 5.015
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES				
Result No.	Score	Query Length	ID	Description
1	202	64.7	400	50 HSI144450
2	176	66.4	412	33 AAC15529

3	176	56.4	418	71 HSI1308877
4	164	52.6	242	26 AA179857
5	164	52.6	242	64 HSI128912
6	164	52.6	324	63 HSI128964
7	164	52.6	324	16 AA164224
8	164	52.6	324	58 HSI126569
9	152	48.7	243	52 HSI1180008
10	152	48.7	243	28 AA181842
11	152	48.7	243	65 HSI1272128
12	148	47.4	255	52 HSI1189086
13	140	44.9	240	29 AA185516
14	140	44.9	240	66 HSI1280478
15	140	44.9	240	57 HSI1227632
16	138	44.2	249	54 HSI1201869
17	136	43.6	242	15 AA144451
18	136	43.6	242	63 HSI1258291
19	136	43.6	269	58 HSI1236090
20	134	42.9	242	29 AA182641
21	134	42.9	242	65 HSI1272927
22	134	42.9	171	63 HSI1267683
23	130	41.7	171	63 HSI1259487
24	129	41.3	251	62 HSI1259487
25	129	41.3	251	16 AA164647
26	120	38.5	217	67 HSI1284569
27	120	38.5	217	38 AA1494059
28	120	38.5	239	50 HSI1149677
29	120	38.5	239	56 AA130271
30	116	37.2	260	27 AA1259588
31	116	37.2	260	49 HSI1143281
32	111	35.6	242	38 AA192131
33	111	35.6	262	68 HSI1290157
34	101	32.4	242	26 AA179833
35	101	32.4	242	64 HSI1268889
36	94	30.1	240	55 HSI121377
37	94	30.1	248	57 HSI1227505
38	88	28.2	363	16 AA164313
39	88	28.2	363	63 HSI1258153
40	84	26.9	297	33 AA195610
41	84	26.9	297	69 HSI1291551
42	78	25.0	442	78 HSA54151
43	63	20.2	335	54 HSI1201911
44	61	19.6	771	13 MMS68M11
45	59	18.6	171	54 HSI1292196

ALIGNMENTS

RESULT 1 standard; RNA: EST: 400 BP.
ID HSI144450 AC AA166778; NI 92177199
DT 07-JUN-1997 (Ref 52, Created)
DT 07-JUN-1997 (Ref 52, Last updated, Version 1)
DE 2427111 r1 Soares Ovary tumor Nbcot Homo sapiens cDNA clone 770541
DE 5' similar to gb:X06764 IG KAPPA CHAIN PPTUPSOR V-11 REGION
DE (HUMAN);
KW Homo sapiens (human)
OS Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP 1-400
PA Hillier L, Allen M, Bowles L, Dubouque T, Gaisel G, Jones S,
Kucaba T, Lamy M, Le N, Lennon G, Marra M, Martin J,
PA Moore R, Schellenberg K, Steptoe M, Tan F, Theisius R,
RA White Y, Wyllie T, Waterston R, Wilson R;
RI "WashU-Merck EST Project 1997";
RL Unpublished.
CC Contact: Wilson PK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC estw@wustl.edu This clone is available royalty-free through
CC LNL: contact the IMA3F Consortium (info@ima3f.org) for

CC further information. Trace considered overall poor quality Seq
 CC primer: -28m13 rev2 ET from Amersham High quality sequence stop: 1.
 FH Key Location/Qualifiers
 FT source 1..400
 FT /organism="Homo sapiens"
 FT /note="organ: ovary; Vector: pT73D (Pharmacia) with a
 FT modified polylinker; Site1: Not I; Site2: Eco RI; 1st
 FT strand cDNA was primed with a Not I - oligo(dT) primer [5'
 FT TGTTACCAATCTGAAGTCGGAGCGCGGTTTCTTTTCTTTTCTTTT
 FT (Pharmacia). Library constructed by Bento Soares and
 FT the Not I and Eco RI sites of a modified pT73 vector
 FT (Pharmacia). Library constructed by Bento Soares and
 FT M Fatima Bonaide
 FT /clone_lib="Soares ovary tumor NBH0T"
 FT /clone="770541"
 FT /sex="female"
 FT /tissue_type="ovarian tumor"
 FT /lab_host="DH10B (ampicillin resistant)"
 FT <1..>400
 FT mRNA
 SQ Sequence 400 BP; 90 A; 120 C; 106 G; 84 T; 0 other;

Query Match 64.7%; Score 202; DB 60; Length 400;
 Best Local Similarity 87.9%; Pred No 0.00e+00;
 Matches 275; Conservative 0; Mismatches 31; Indels 7; Gaps 5;

Db 70 acgagctccagggaccctgtctgtctccagggaggaagagccacctctctcagc 129
 QY 7 ACTCAGTCTCCAGCCACCCCTGCTTTGTCTCCAGGGGAAAGAGCCACCTCTCTG 66

Db 130 gcagctccagctgttagcagcagctgttagcctgtaccagcaggaacacctggccagct 189
 QY 67 GCCAGTCAGAGTGTAAACA--AG-TACTTAGCTGTGTACCAAGCAACCTTGGCAGGCT 123

Db 190 ccagagctctctctatctgtgtcctccagcagggcaactggcctccagcagcagcttcagct 249
 QY 124 CCCAGGCTCTCTATCTATGATGATCCACAGAGGCTGATGATGATGATGATGATGAT 183

Db 250 ggcagtggtgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 309
 QY 184 GGCAGTGCTGTCTGT 242

Db 310 tgcagtgattactgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 369
 QY 243 TGCAGTTTATTACTGTGAGCAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 299

Db 370 ggtggaaatcaaa 382
 QY 300 GGTGGAGATCAAA 312

RESULT 2
 LOCUS AA515239 418 bp mRNA EST 14-JUL-1997
 DEFINITION g959c07.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone 940044 similar to
 gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
 ACCESSION AA515239
 NID 92254839
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 Homo.
 1 (bases 1 to 418)
 NCI-CGAP
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINK at:
 www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m13 fwd, ET from Amersham
 High quality sequence stop: 413.

FEATURES
 source

location/Qualifiers

1..418

/organism="Homo sapiens"

/note="Vector: pAMP10; mRNA made from liposarcoma. cDNA

made by oligo-dT priming. Non-directionally cloned.

Size-selected on agarose gel, average insert size 600 bp.

Reference: Krizman et al. (1996) Cancer Research

56:5380-5383.

/clone="940044"

/clone_lib="NCI_CGAP_Lip2"

/tissue_type="liposarcoma"

/lab_host="DH10B"

<1..>418

90 a 127 c 102 g 90 t

mRNA

BASE COUNT

ORIGIN

Query Match 56.4%; Score 176; DB 39; Length 418;
 Best Local Similarity 87.7%; Pred No 3.54e+297;
 Matches 228; Conservative 0; Mismatches 28; Indels 4; Gaps 3;

Db 95 acgagctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 154
 QY 7 ACTCAGTCTCCAGCCACCCCTGCTTTGTCTCCAGGGGAAAGAGCCACCTCTCTG 66

Db 155 gccagctcagctatctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 214
 QY 67 GCCAGTCAGAGTGTAAACA--AGTAC-TTAGCTGTGTACCAAGCAACCTGCCCCAGGCT 123

Db 215 ccagagctctctctatctcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 273
 QY 124 GGCAGTGCTGTCTGT 183

Db 274 ggcagctcgtcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 333
 QY 184 GGCAGTGCTGT 243

Db 334 gcagtttactattgtcagca 353
 QY 244 GCAGTTTATTACTGTCTCAGCA 263

RESULT 3

ID HS1308877 standard; RNA; EST; 418 BP.

AC AA515239;

NI 92254839

DT 15-JUL-1997 (Rel. 52, Created)

DT 24-JUL-1997 (Rel. 52, Last updated, Version 2)

DE g959c07.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone 940044 similar to

DE gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);

KW EST.

OS Homo sapiens (human)

OC Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

OC Homo.

RN [1]

RP 1-418

RA NCI-CGAP;

RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

RT Tumor Gene Index";

RL Unpublished;

CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:

CC Robert_Strausberg@nih.gov Tissue Procurement: L. Jeffrey Medeiros,

M.D., Michael P. Emerit-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lenson, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Cloning Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/UMI at: www.bio.tlni.gov/tlrf/image/ Image Bank Insert Length: 1070 Std Error: 0.00 Seq primer: -40m3 fwd, EI from Amersham High quality sequence stop: 413. Location/Qualifiers

FFH source 1..418
FFH /organism="Homo sapiens"
FFT /note="Vector: pAMP10; mRNA made from liposarcoma, cDNA made by oligo-dT priming. Non- directionally cloned."
FFT Size-selected on agarose gel, average insert size 600 bp.
FFT Reference: Krizman et al (1995) Cancer Research 56:5380-5383
FFT /clone="940044"
FFT /clone_lib="NCI_CGAP_Lip2"
FFT /tissue_type="liposarcoma"
FFT /lab_host="DH10B"
FFT GI:2478

FFH mRNA
FFH Sequence 418 BP: 99 A; 127 C; 102 G; 90 T; 0 other;
FFH Best Local Similarity 56.4%; Score 176; DB 71; Length 418;
FFH Query Match 87.7%; Pred No 3,59e-297;
FFH Mismatches 229; Conservative 0; Mismatches 28; Indels 4; Gaps 3;

95 accgaggtctcagggagacacctctctcttctctcaggggaaagagatccacctctcttttcagg 154
96 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
97 ACTCAGCTTCTAGTACAG 69
98 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
99 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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173 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
174 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
175 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
176 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
177 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
178

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Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL : contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer -28ml3 rev2 EF from Amersham.
Location/Qualifiers
Source
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/note="Organ: ovary; Vector: p77TD (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5'-
TGTTACCAATCTCAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTT 3']."
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
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(Pharmacia) Library constructed by Bento Soares and
M.Patima Bonaldo."
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/lab_host="DH1CB (ampicillin resistant)"
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/db_xref="GBD:5939539"
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Query Match 52.6% Score 164 DB 266 Length 242
Best Local Similarity 91.4% Pred. No. 1,59e-272
Matches 20%, Conservative 6%, Mismatches 1%, Indels 4%, Gaps 2%

DB 21 tacttgagctggtacgaacgaagaacttgcggcgcccaaggcgtatggtatggcacacacttc 80
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 88 TACTTAGGTTCGTATCATTAATGAAATATGAGCAGATGATGAGAGCTGCATGATGATGATGAT 147
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DB 81 ttccaccagggccacctgcatccatcacaggtttccattgacagtggatgggatggcacacacttc 140
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 148 TTCAAACAAGGTCATGGCATATTGATATGATGATGATGATGATGATGATGATGATGATGATG 207
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DB 141 actctccaccatcagcagctggtggtcctaagaatttcagctgatatattctatgccagcata 200
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QY 209 ATTCTCAATATA-GAAGAATTAATATTTAAATATTTGAATATTAATATTAATATTAATATTA 265
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DB 201 tggtagctcacgcctcactcttcggcggaaggagggaccaaggtgga 242
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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AC AA479857;
N1 Q2205743
DT 23-JUN-1997 (Rel. 52, Created)
DI 23-JUN-1997 (Pel. 52, Last updated, Version 1)
DE zu35B05.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 739953
DE 5' similar to gb:X86754.15 KAPPA CHAIN PEPTIDOPOR V-II REGION
DE (HUMAN)?
DE KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
[1]
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RA Hillier L., Allen M., Bowles L., Dubouque T., Giesel G., Post S.,
RA Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
RA Martin J., Moore R., Schellenberg K., Steptoe M., Tan F.,
RA Theising R., White Y., Willie T., Waterston P., Wilson R.:
RA "Wash-NOT human EST Project".
RL Unpublished.
CC Contact: Watson PK Washington University School of Medicine 4444
CC Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286
CC 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is

```

```

Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL : contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer -28ml3 rev2 EF from Amersham.
Location/Qualifiers
Source
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/note="Organ: ovary; Vector: p77TD (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'-
TGTTACCAATCTCAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTT 3']."
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTZ19 vector
(Pharmacia) Library constructed by Bento Soares and
M.Patima Bonaldo."
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/lab_host="DH1CB (ampicillin resistant)"
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54 a 56 c 69 g 53 t

BASE COUNT
ORIGIN
Query Match 52.6% Score 164 DB 266 Length 242
Best Local Similarity 91.4% Pred. No. 1,59e-272;
Matches 20%, Conservative 6%, Mismatches 1%, Indels 4%, Gaps 2%

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QY 209 ATTCTCATATCA-GCAAATTAAATGCTTAATATTTTAAATTTTAAATTTTAAAT 265
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QY 266 --GTAGGAGAGTGGGTGCACTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 305
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DI 23-JUN-1997 (Pel. 52, Last updated, Version 1)
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DE (HUMAN)?
DE KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RP 1-242
RA Hillier L., Allen M., Bowles L., Dubouque T., Giesel G., Post S.,
RA Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,
RA Martin J., Moore R., Schellenberg K., Steptoe M., Tan F.,
RA Theising R., White Y., Willie T., Waterston P., Wilson R.:
RA "Wash-NOT human EST Project".
RP Unpublished.
RL Contact: Watson PK Washington University School of Medicine 4444
OC Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286
OC 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is

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/lab_host="DH10B (ampicillin resistant)"					
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Best Local Similarity 97.5%; Pred No 5.45e-248;					
Matches 156; Conservative 0; Mismatches 4; Indels 0; Gaps 0;					
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Db	144	gccatccagagtgttagcagctactctagcttggtaccacagaacaactggccagggtccc	203		
QY	67	GCCAGTCAAGTGTTAACAAGACTTATAGCTGTGTACCAAGAGAAGCTGGCTAGGCTGCG	126		
Db	204	aggctcccatctgatcgatccatccaacagggccactggca	243		
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AC	AA481842:				
NI	q2209520				
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DE	24-JUN-1997	(Rel. 52, Last updated, Version 1)			
DEFN	zv42c03.r1 Soares ovary tumor NBH07 Hom sapiens cDNA clone 756292				
KEYW	5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-II REGION				
FE	(HUMAN);				
OC	Homo sapiens (human)				
OS	Homo sapiens (human)				
OC	Eukaryota; Eukarya; Metazoa; Chordata;				
OC	Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.				
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RP	1-243				
RA	Hillier L., Allen M., Bowles I., Dubouque T., Geisler G., Host S.,				
RA	Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M.,				
RA	Martin J., Moore B., Schellenberg K., Steptoe M., Tan F.,				
RA	Theising B., White Y., Wylie T., Waterston P., Wilson P.;				
PT	"Washington Human EST Project";				
RL	Unpublished.				
RC	Contact: Washington University School of Medicine 4444				
CC	Forest Park Parkway, Box 8501, St Louis, MO 63108 Tel.: 314 286				
CC	1800 Fax: 314 286 1810 Email: estatstoun.wustl.edu This clone is				
CC	available royalty-free through INM; contact the IMAG Consortium				
CC	(info@image.lln.gov) for further information. Seq primer: -28ml3				
CC	rev2 E1 from Amersham.				
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FT	/note="Organ: ovary; Vector: pT713D (Pharmacia) with a				
FT	modified polylinker. Site: Not I, Site2: Eco RI; 1st				
FT	strand cDNA was primed with a Not I - oligo(drf) primer [5,				
FT	TGTTACCAATTGAAGTGAAGCGGCGGGGTTTTTTTTTTTTTTT 3'].				
FT	double-stranded cDNAs size selected, ligated to Eco RI				
FT	adapters (Pharmacia), digested with Not I and cloned into				
FT	the Not I and Eco RI sites of a modified pT73 vector				
FT	(Pharmacia). Library constructed by Renato Soares and				
FT	M Fatima Bonaldo."				
FT	/clone="756292"				
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FT	/tissue_type="ovarian tumor"				
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FT	<1..>243				
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Sequence	243 BP; 56 A; 81 C; 56 G; 50 T; 0 other;				
Query Match 48.7%; Score 152; DB 65; Length 243;					
Best Local Similarity 97.5%; Pred. No. 5.45e-248;					

WILEY

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPSrch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:39:26 1998; Master time 107.99 seconds
Tabular output not generated. 814 795 Million cell updates/sec

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Description: (1-312) from US08844215.seq
Perfect Score: 312
N.A. Sequence: 1 GAGTCACATCAGCTCCAGC
Comp: CACGAGTGAGTCAGAGTTC
GAGCAGAGCTGAGATGAAA 312
GAGTCACATCAGCTCCAGC
CACGAGTGAGTCAGAGTTC

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 39746 seqs. 141010104 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-C
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7:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208
13:EST209 14:EST210 15:EST211 16:EST212 17:EST213
18:EST214 19:EST215 20:EST216 21:EST217 22:EST218
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119:EST315

Statistics: Mean 9.871; Variance 1.938; scale 5.0q3
Pred. No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	224	71.8	328	24	AA295311	EST100471 Pancreas tu
2	218	69.9	370	24	AA295093	EST100400 Pancreas tu
3	212	67.9	349	59	AA457044	EST101406 Skin tumor
4	202	64.7	400	116	AA457078	EST101411 Skin tumor
5	189	63.5	346	25	AA300582	EST13427 Testis tumor
6	188	63.5	363	55	AA367405	EST174511 Pancreas tum
7	189	60.6	405	52	AA360223	EST69341 lymph node
8	188	60.6	403	73	AA364586	EST151505 Gall bladder
9	184	52.6	283	53	AA461678	EST101165 Thymus
10	163	51.2	253	25	AA395941	EST101165 Thymus
11	159	51.0	238	62	AA382014	EST101165 Thymus
12	157	50.3	277	24	AA395377	EST100538 Pancreas tu
13	155	49.7	289	37	AA327218	EST105586 Colon
14	152	48.7	330	87	AA434180	EST27610 SL Soares ova
15	152	48.7	343	50	AA324584	EST23111 SL Soares ova
16	152	48.7	343	83	AA422182	EST31503 SL Soares ova
17	151	48.4	294	55	AA365451	EST17408 Pancreas tum
18	148	47.4	255	92	AA384662	EST24303 SL Soares ova
19	148	47.4	264	24	AA295154	EST100323 Pancreas tu
20	145	46.8	253	100	AA291691	EST36012 SL Soares ova
21	140	44.9	244	86	AA430565	EST23009 SL Soares ova
22	138	44.2	249	79	AA432152	EST56951 SL Soares ova
23	137	43.9	345	39	AA335885	EST19457 Esophagus tu
24	135	43.6	259	87	AA434001	EST51012 SL Soares ova
25	134	42.9	255	100	AA294047	EST50122 SL Soares ova
26	132	42.3	252	27	AA301361	EST14181 Testis tumor
27	130	41.7	357	53	AA361497	EST10401 T-cell lymph
28	126	40.4	413	27	AA301347	EST14272 Testis tumor
29	125	40.1	382	25	AA355866	EST100947 Pancreas tu
30	124	39.7	306	100	AA291710	EST36012 SL Soares ova
31	122	39.1	304	100	AA294299	EST36012 SL Soares ova
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33	116	37.2	260	71	AA325858	EST27095 SL NC1 GAP P
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36	111	35.6	303	26	AA300598	EST13348 Testis tumor
37	110	35.3	303	26	AA400891	EST14041 Testis tumor
38	109	34.9	333	26	AA300732	EST13847 Testis tumor
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Immunoglobulin kappa light chain, VJ regions.
ACCESSION AA295311
NID g1947646
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 328)
AUTHORS Adams, M.P., Verlavage, A.P., Fleischmann, P.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Socolay, J.D.,
White, C., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, I.R., Cotton, M.D., Earle-Hughes, J., Fine, L.B.,
Fitzgerald, L.M., Fitzhugh, W.M., Frichman, J.B., Geachagan, N.S.,
Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkley, P.S., J.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (5547 Suppl.), 3-174 (1995)
96026280
Other ESTs: THC169106
Contact: KeriAvage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arker@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the tigr Human Gene index (<http://www.tigr.org/tdb/hgi/hgi.html>)
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TGTTACCAATCTCAAGTCGGACGGCCCGTTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
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M.Fatima Bonaldo."
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90 a 120 c 106 g 84 t

mrna

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QY 184 GGCAGTGGTCTGAGACAGACATTCATCTTCACTCACTCACTCACTCACTCACTCACT 242

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QY 300 GTTCGAGATCAAA 312

RESULT 5
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ACCESSION AA300582
NID G1952925
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,R.D., Fuldner,P.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C., Clayton,P.A., Cline,T.P., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Pyder,S.E., Scott,J.T., Saudex,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,T.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hangjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.F., Posen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other_ESTs: THCL69106
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
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/clone_lib="Testis tumor"
/sex="male"
/dev_stage="adult"

FEATURES
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QY 67 GCCAGTCAGAGTGTAAACA--AG-TACTTAGCTGTGTACCAACAGAAACCTGGCCAGGCT 123

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Db 250 qccagtggtctgagacagacttcaactcaacatcgccagagctggagcctgacgattt 309

QY 184 GGCAGTGGTCTGAGACAGACATTCATCTTCACTCACTCACTCACTCACTCACTCACT 242

Db 310 tgcagtgattatctgacagcagatggtgtagctccacgtgagcgttgcgcgaaggagccca 369

QY 243 TGCAGTATTATCTACAGCAGGCTAGGAGCTGAG--GTC--ATTTCGTGCTGAGGAGCTAA 299

Db 370 ggtgggaatcaaa 382

QY 300 GTTCGAGATCAAA 312

RESULT 6
LOCUS AA367405 363 bp mRNA EST 21-APR-1997
DEFINITION EST78511 Pancreas tumor III Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain.
ACCESSION AA367405
NID G2019753
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C., Clayton,P.A., Cline,T.P., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Pyder,S.E., Scott,J.T., Saudex,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,T.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hangjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.F., Posen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other_ESTs: THCL69106
Contact: Kerlavage, AR
Bioinformatics
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Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1..346
/organism="Homo sapiens"
/note="Organ: testis; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
/clone_lib="Testis tumor"
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/dev_stage="adult"

FEATURES
source

QY 67 GCCAGTCAGAGTGTAAACA--AG-TACTTAGCTGTGTACCAACAGAAACCTGGCCAGGCT 123

Db 190 CCAGGCTCTCTATAGTATCATCCAGGGAAGCAAGTGCATCCCAAGCAGGATTCAGT 249

QY 124 CCAGGCTCTCTATAGTATCATCCAGGGAAGCAAGTGCATCCCAAGCAGGATTCAGT 183

Db 250 qccagtggtctgagacagacttcaactcaacatcgccagagctggagcctgacgattt 309

QY 184 GGCAGTGGTCTGAGACAGACATTCATCTTCACTCACTCACTCACTCACTCACTCACT 242

Db 310 tgcagtgattatctgacagcagatggtgtagctccacgtgagcgttgcgcgaaggagccca 369

QY 243 TGCAGTATTATCTACAGCAGGCTAGGAGCTGAG--GTC--ATTTCGTGCTGAGGAGCTAA 299

Db 370 ggtgggaatcaaa 382

QY 300 GTTCGAGATCAAA 312

RESULT 6
LOCUS AA367405 363 bp mRNA EST 21-APR-1997
DEFINITION EST78511 Pancreas tumor III Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain.
ACCESSION AA367405
NID G2019753
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C., Clayton,P.A., Cline,T.P., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Pyder,S.E., Scott,J.T., Saudex,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,T.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hangjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.F., Posen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
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Contact: Kerlavage, AR
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone_lib="Testis tumor"
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FEATURES
source

Small, K. V., Spriggs, T. A., Unterback, T. R., Weidman, J. F., Li, Y.,
Bednarik, D. P., Cao, L., Cepeda, M. A., Coleman, T. A., Collins, E. J.,
Dimke, D., Feng, D. F., Ferrile, A., Fischer, C., Hastings, G. A.,
He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P. S., Kim, A. K.,
Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Weissner, P. S., Olsen, H.,
Raymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M.,
Dillion, P. J., Fannon, M. P., Rosen, C. A., Haseltine, W. A., Fields, C.,
Fraser, C. M. and Venter, J. C.

Initial assessment of human gene diversity and expression patterns
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96026280

Contact: Kerlavage, AR
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Fax: 3018699423

Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tadb/hgi/hgi.html>)
Seq primer: M13 Reverse.

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BASE COUNT

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RESULT 9
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DEFINITION EST70983 T-cell lymphoma Homo sapiens cDNA 5' end similar to
similar to immunoglobulin kappa, variable region (GB:Y00640).
ACCESSION AA361678
NID g2013998
KEYWORDS EST
SOURCE Human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Hominidae;
Homo.

REFERENCE

AUTHORS
1 (bases 1 to 283)
Adams, M. D., Kerlavage, A. P., Fleischmann, R. D., Fullmer, R. A.,
Bult, C. J., Lee, N. H., Kirkness, F. F., Weinstock, K. G., Gocayne, J. D.,
White, O., Sutton, G., Blake, J. A., Brandon, R. C., Man-Wai, C.,
Clayton, R. A., Cline, T. R., Cotton, M. D., Earle-Hughes, J., Fine, L. D.,
Fitzgerald, L. M., Fitch, W. M., Fritchman, J. L., Geoghegan, N. S.,
Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Jr.,
Kelley, J. M., Kelley, J. C., Liu, J. I., Marmaros, S. M., Merrick, J. M.,
Moreno-Palauques, R. F., McDonald, L. A., Nguyen, P. T., Pelligrino, S. M.,
Phillips, C. A., Ryder, S. E., Scott, J. L., Sandek, D. M., Shirley, R.,
Small, K. V., Spriggs, T. A., Unterback, T. R., Weidman, J. F., Li, Y.,
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He, W. W., Hu, J. S., Greene, J. M., Gruber, J., Hudson, P. S., Kim, A. K.,
Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Weissner, P. S., Olsen, H.,
Paymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G. L., Ruben, S. M.,
Dillion, P. J., Fannon, M. P., Posen, C. A., Haseltine, W. A., Fields, C.,
Fraser, C. M. and Venter, J. C.

TITLE

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280

JOURNAL

MEDLINE

COMMENT

Other ESTs: TIGR168243

Contact: Kerlavage, AR

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Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tadb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

SOURCE

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283
58 a 90 c 72 g 59 t 4 others

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ORIGIN

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Matches 179; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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QY 194 CTGGGACAGACTTCACCT 210

RESULT

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

10
AA295941 253 bp mpna EST 18-APP-1997
EST101165 Thymus II Homo sapiens cDNA 5' end similar to
immunoglobulin kappa light chain, V region (GB:Y00640).
AA295941
q1948286
EST.

QY 195 T 195

RESULT 12
LOCUS AA295377 277 bp mRNA EST 18-APR-1997
DEFINITION EST100538 Pancreas tumor 1 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VJ regions.
ACCESSION AA295377
NID g1947711
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondria; eukaryotes; Metazoa; Chordata.
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 277)
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gockayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geodhagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligriano, S.M., Phillips, C.A., Rydger, S.E., Scott, J.L., Saudek, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarek, D.P., Feng, D.-F., Fierrie, A., Fischer, J., Collins, E.J., Dimke, D.L., Peng, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., He, W.W., Hu, J.S., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, T., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Pannon, M.F., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
Other ESTs: THCL69106
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the tigr Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)
Seq primer: M13 Reverse

FEATURES
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Best Local Similarity 91.4%; Prod. No. 2,870,262;
Matches 191; Conservative 0; Mismatches 14; Indels 4; Gaps 3.

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Qb 130 gccagctcagagctttagcagcagctacttagcctggtaccagcagaaacccctggccagcgt 189
QY 67 GCCAGTCAGAGCTGTTAACA-AG-TACTTAGCTGTGTACACAGAAACCTGTCAGGCT 123

Db 190 ccagntctctcatctatgttgatccagagaggccactggnatccacagaggttcagt 249
QY 124 CCCAGGCTCTCATCTATGATGATCCCAACAGAGGACAGTGGCATCCACAGCTTCAGT 183

Db 250 ggcagtggtctggagacg-cttcaactct 277
QY 184 GGCAGTGGGTCTGGACAGACTTCACTCT 212

RESULT 13
LOCUS AA327218 289 bp mRNA EST 30-APR-1997
DEFINITION EST30586 Colon 1 Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VNI regions (GB:Z11894).
ACCESSION AA327218
NID g1979524
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondria; eukaryotes; Metazoa; Chordata.
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 289)
AUTHORS Adams, M.D., Kerlavage, A.P., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gockayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geodhagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligriano, S.M., Phillips, C.A., Rydger, S.E., Scott, J.L., Saudek, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarek, D.P., Feng, D.-F., Fierrie, A., Fischer, J., Collins, E.J., Dimke, D.L., Peng, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Paymend, L., Wei, Y.F., Wing, T., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Pannon, M.F., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
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Contact: Kerlavage, AR
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Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the tigr Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)
Seq primer: M13 Reverse

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QY 127 AGGCTCCTCATCTATGATGCATCCCAACAGGGCCACTGGCA 166

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Job time : 173 secs.

W O R L D

(TM)

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MPsearch_n.a - n.a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:34:25 1998 Maspar time 198 19 seconds
818.703 Million cell updates/sec

Tabular output not generated.

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Comp: CTCAGTACGTCAGAGGCTC... CTCAGTACGTCAGTACGTT

Scoring table: TABLE default
Gap 5

Nmatch STD Dbase C. Query C

Searched: 555793 seqs 246912990 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Database: EST-B
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104-EST104 105-EST105 106-EST106 107-EST107 108-EST108
109-EST109 110-EST110 111-EST111 112-EST112 113-EST113
114-EST114 115-EST115 116-EST116 117-EST117 118-EST118
119-EST119 120-EST120 121-EST121 122-EST122 123-EST123
124-EST124 125-EST125 126-EST126 127-EST127 128-EST128
129-EST129 130-EST130 131-EST131 132-EST132 133-EST133
134-EST134 135-EST135 136-EST136 137-EST137 138-EST138
139-EST139 140-EST140 141-EST141 142-EST142 143-EST143
144-EST144 145-EST145 146-EST146 147-EST147 148-EST148
149-EST149 150-EST150 151-EST151 152-EST152 153-EST153
154-EST154 155-EST155 156-EST156 157-EST157 158-EST158
159-EST159 160-EST160 161-EST161 162-EST162 163-EST163
164-EST164 165-EST165 166-EST166 167-EST167 168-EST168
169-EST169 170-EST170 171-EST171 172-EST172 173-EST173
174-EST174 175-EST175 176-EST176 177-EST177 178-EST178

Statistics: Mean 9.906; Variance 1.931; scale 5.129

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description	Prod. No.
1	216	69.2	332	59	T29342	EST77461 Homo sapiens	0.000-00
2	213	68.3	453	34	P69532	Y18109.1 Homo sapiens	0.000-00
3	203	65.1	381	58	T29114	EST69430 Homo sapiens	0.000-00
4	183	58.7	393	54	T29478	EST14907 Homo sapiens	0.000-00
5	183	58.7	383	59	T29016	EST00071 Homo sapiens	0.000-00
6	183	58.7	385	64	H26475	Y18106.1 Homo sapiens	0.000-00
7	182	58.3	451	10	T29236	Y18109.1 Homo sapiens	0.000-00
8	171	54.9	570	34	P70290	Y18109.1 Homo sapiens	4.700-293
9	161	51.6	359	64	H27642	Y18109.1 Homo sapiens	4.420-272
10	158	50.6	401	40	P10529	Y18106.1 Homo sapiens	8.360-266
11	153	49.0	360	37	P79407	Y18109.1 Homo sapiens	2.320-255
12	153	49.0	460	64	H44749	Y18109.1 Homo sapiens	2.320-255
13	149	47.8	361	28	R19122	Y18109.1 Homo sapiens	5.050-247
14	134	42.9	393	58	T27593	EST100653 Homo sapiens	5.470-216
15	133	42.6	218	54	H27031	Y18109.1 Homo sapiens	7.760-214
16	138	41.0	171	64	H25498	Y18109.1 Homo sapiens	1.590-203
17	136	40.4	232	63	H21646	Y18109.1 Homo sapiens	2.070-199
18	131	38.9	161	63	H22088	Y18109.1 Homo sapiens	2.070-199
19	118	37.9	176	61	H44909	Y18109.1 Homo sapiens	2.360-189
20	116	37.2	421	27	H48043	Y18109.1 Homo sapiens	2.360-189
21	115	36.9	447	89	H70726	Y18109.1 Homo sapiens	7.010-177
22	115	36.9	516	33	R67559	Y18109.1 Homo sapiens	7.010-177
23	110	35.3	395	58	T29112	EST69384 Homo sapiens	1.060-166
24	110	35.3	438	33	R64593	Y18109.1 Homo sapiens	1.060-166
25	106	34.0	237	65	H28991	Y18109.1 Homo sapiens	1.360-154
26	97	31.1	201	64	H26206	Y18109.1 Homo sapiens	1.360-154
27	97	31.1	434	11	T31178	Y18109.1 Homo sapiens	1.850-140
28	96	30.8	503	22	R28232	Y18109.1 Homo sapiens	1.850-140
29	93	29.8	279	59	T29056	EST89211 Homo sapiens	1.850-140
30	93	29.8	290	46	H45841	Y18109.1 Homo sapiens	1.850-140
31	92	29.5	470	81	H20115	Y18109.1 Homo sapiens	1.850-140
32	91	29.2	289	58	T27591	EST100107 Homo sapiens	1.790-128
33	91	29.2	354	58	T27579	EST100349 Homo sapiens	1.790-128
34	90	28.8	488	64	H25625	Y18109.1 Homo sapiens	1.790-128
35	89	28.5	288	58	T27721	EST13441 Homo sapiens	1.790-128
36	94	27.9	210	34	R69482	Y18109.1 Homo sapiens	1.790-128
37	94	27.9	170	69	H44238	Y18109.1 Homo sapiens	1.790-128
38	93	26.6	189	51	R29213	Y18109.1 Homo sapiens	1.790-128
39	78	25.0	438	34	R25535	Y18109.1 Homo sapiens	1.790-128
40	77	24.7	467	64	H27034	Y18109.1 Homo sapiens	1.790-128
41	73	23.4	213	64	H25521	Y18109.1 Homo sapiens	1.790-128
42	72	23.1	405	27	R48845	Y18109.1 Homo sapiens	1.790-128
43	71	22.9	359	58	T27597	EST100475 Homo sapiens	1.790-128
44	69	22.1	262	60	H44273	Y18109.1 Homo sapiens	1.790-128
45	68	21.9	397	34	P70292	Y18109.1 Homo sapiens	1.790-128

ALIGNMENTS

1 T29342 332 bp mRNA EST 06-SEP-1995
LOCUS EST77461 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
DEFINITION light chain, V region (CR-M29469) (H13056).
ACCESSION T29342
NID G611440
KEYWORDS EST
SOURCE human primer-M13 Reverse library-Human Factor-35.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 332)
ADAMS, M.D., Keriavage, A.P., Fleischmann, P.D., Fuldner, P.A., Buit, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Sutton, G., Blake, J.A., Brannon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitz-Gerald, J.M., Fitz-Hugh, W.M., Fritchman, T.L., Geoghagen, N.S.M., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, Jr., P.S., Kelley, J.M., Klemke, K.M., Kelley, J.C., Lib, L.-I., Marmaro, S.M., Merrick, J.M., Moreno-Palauques, P.F., McDonald, L.A., Nguyen, P.T., Pellegrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L., Saudek, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferris, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Li, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Puker, S.M., Dillon, P.J., Pannon, M.P., Posen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
JOURNAL Based Upon 52 Million Basepairs of cDNA Sequence
COMMENT Other ESTs: THC22876
Contact: Venter, J.C.
The Institute for Genomic Research
932 Clopper Rd. Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@db.tigr.org).

FEATURES
Source 1..332
/organism="Homo sapiens"
/clone="155249"
BASE COUNT 75 a 100 c 74 g 76 t 7 others
ORIGIN
Query Match 69.2% Score 213; DB 58; Length 332;
Best Local Similarity 95.1% Pred NO 0.00e+00;
Matches 234; Conservative 0; Mismatches 10; Indels 2; Gaps 2.
Db 82 acacatctccagccacctgtttgttctccaggggaagagccacctctctcgtcagg 141
|||
QY 7 ACTCAGTCTCCAGCCACCTGTTTGTCTCCAGGGGAAGAGCCACCTCTCTCGAGG 66
Db 142 gcaatcgaacttttaggaacttaacttgccttggtaccagcaagaacagccaggtccc 201
|||
QY 67 GCCAGTCAGAGTGTAAACAAGTACTTAGCTGTGTACCAACAGAAACCTGGGCTCC 126
Db 202 aggtcctcatctatgatcatcccaacagggccactggtccatccagccaggttcagttgc 261
|||
QY 127 AGCTTCCTATCATCATGCATCCCAACAGGCGCACTGCATCCCAACAGGCTTCAGTGGC 186
Db 262 agtggctctnagagacacttttcaactcttnaccatcagcagccttagagcattttg 321
|||
QY 187 AGTGGCTCTGGACACACTT-CAGTCT-CAGCATCAGCAACCTAGAGCCTGAAGATTTG 244
Db 322 gatttt 327
|||
QY 245 CAGTTT 250

RESULT 2
LOCUS 463 bp mpNA EST 01-JUN-1995
DEFINITION Y182d09.21 Homo sapiens cDNA clone 155249, similar to gp-M53438
IG KAPPA CHAIN PRECURSOR V-111 REGION (HUMAN);
ACCESSION R59532

9843049
EST.
human clone=155249 library=Soares breast 2NHRer vector=pf7T3D
(Pharmacla) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13p21 F51e1-Not I R51e2-Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAATGGAGGAGGCGCCCTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacla). Library went through one round
of normalization to a Cot = 230 Library constructed by Hon'o
Soares and M.Patina Bonaldo.
Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 463)
HILLER, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kuraba, T., Le, M., Lennon, G., Rarrad, M., Parsons, J., Rifkin, L., Rohlfing, J., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 9501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 394
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
Source 1..463
/organism="Homo sapiens"
/clone="155249"
BASE COUNT 103 a 125 c 115 g 114 t 6 others
ORIGIN
Query Match 68.3% Score 213; DB 34; Length 463;
Best Local Similarity 90.2% Pred NO 0.00e+00;
Matches 238; Conservative 0; Mismatches 26; Indels 0; Gaps 0.
Db 89 ctccagccacctgtgtgtctctccaggggaagagccacctctctcagagccagtc 148
|||
QY 14 CTCAGCCACCTCTCTTGTCTCCAGGGGAAGAGCCACCTCTCTCTCTCTCTCTCT 73
Db 149 agactgtgagcttaaatattagcttggtaccagcagcaaaactgagcaggtcccaggtcc 208
|||
QY 74 AGAGTGTAAACAAGTACTTAGCTGTGTACCAACAGAAACCTGGGCTCC 133
Db 209 tcaatctatgttggtatccacaggggacctggtatccacagcaggttcagtgccagttggt 268
|||
QY 134 TCATCTATGATGATCATCAACAGAGGCACTAGCATCCCAACAGGCTTCAGTGGTATGAT 193
Db 269 ctggagacagattctttctcaccatcagcagcctgagcctaaagattttgagattatt 328
|||
QY 194 CTGGGACAGATTCAGTCTCTCAGCATCAGCAACCTAGAGCCTGAAGATTITATT 253
Db 329 attctcagcaataataattactgg 352
|||
QY 254 ACTGTCAGTACAGTACGAGTACTGGG 277

RESULT 3
LOCUS 381 bp mpNA EST 06-SEP-1995
DEFINITION EST69430 Homo sapiens cDNA 5' end similar to immunoglobulin light
chain V(L11).J(V) regions (CE-22770) (HT-3121).

2

```

325 ttgcagtttatt 336
I | |||||
343 T-GAGATTATT 253

RESULT      8   P70200    570 bp     MPNA          EST       C1-JUN-1995
ACCESSION  YJ81008.r1 Homo sapiens cDNA clone 155151 5' similar to ab:X05744
DEFINITION IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN) ;
ACCESSION  R70290
KEYWORDS   g843807
SOURCE     Human clone-155151 library-Soares breast 2Nbreast vectorap773D
           (Pharmacla) with a modified polylinker host-DHI0B (ampicillin
           resistant) primer-M13P1 Psitg1-Not I Psite2-Eco RI Adult female.
           1st strand cDNA was primed with a Not I - oligo(dT) primer [5'.
           TGTTACCATGTCGAAGTGAGCGGCCGCCTTTTTTTTTTTT 3'].
           double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla),
           digested with Not I and cloned into the Not I and Eco RI sites of a
           modified pVII3 vector (Pharmacla). Library went through one round
           of normalizatiion to a tot = 240. Library constructed by Bento
           Soares and M Fatima Ronaldo

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Elumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominoideae; Homo.
REFERENCE  1 (bases 1 to 570)
AUTHORS   Hillier,L , Clark,N , Dubuyue,T , Flliston,K , Hawkins,M.,
            Holman,M , Hultkan,M , Kucaba,T , Le-M , Lennon,G., Marra,M.,
            Parsons,J , Rifkin,L , Rohlfing,T , Soares,M., Tan,F.,
            Traverskiis,P , Waterston,R , Williamson,A , Wohlmann,P. and
            Wilson,R.
TITLE      The WashU-Merck EST Project
JOURNAL    Unpublished (1995)
COMMENT    Contact: Wilson PK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 285 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 316
            Source: IMAGE Consortium, LNL
            This clone is available royalty-free through LNL : contact the
            IMAGE Consortium (info:image@lnl.gov) for further information.
FEATURES   Location/Qualifiers
            source             1..570
                               /organism="Homo sapiens"
                               /clone="155151"
BASE COUNT 122 a 140 c 141 g 149 t 18 others
ORIGIN

Query Match      54 8% Score 171 DB 34 Length 570;
Seq Local Similarity 87 5%, Prob Neg 4.70e-23;
Matches 255; Conservative 0; Mismatches 27; Indels 5; Gaps 4;

Ddb      93 acgcagcttcagggaacccgttgtttgttcgggggaagaagcaccctctcctgcagg 152
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      7 ACTCAGTCCAGCACCCGTGTCTTTGTCTCCAGGGGSAAGACCATCTCTCTGTCAGG 56

Ddb      153 tcacgtcaggttgtaacagcaactctttaagctgtatccacaagaagctcgagccac 212
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      67 GCCAGTCAGAGTGTAAACA---ASLACTTAGCCCTGGSIATCAACAGAAATCTGSGTAGGCT 128

Ddb      213 ccgcgtctcccatcttgttgtagcatcccaggaccacctgatctnccaacaaatctcg 272
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      124 CCCAGGCTCCCTCATCTAATGATG-CATCCAACAGGGCCATCTGGCAT--CCAGCCAGGATTA 161

Ddb      273 gtggcagtggtgtgggacacactcttacctctgcctgcagcagcagcagcagcagcagc 332
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

QY 182 GTGGCACTGAGTCTGGAGAGATTTCATCTCACCATCAGCAACCTAGAGGCTGAGATT 241
 Db 333 ttgacctgtattactat 349
 QY 242 TTGCACTTATTACTGT 258

RESULT 9
 LOCUS H27642 359 bp mRNA EST 13-JUL-1995
 DEFINITION Y161q07 r1 Homo sapiens cDNA clone 162780 5' similar to gb.X06764
 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
 ACCESSION H27642
 NID 9897995
 KEYWORDS EST.
 SOURCE human clone=162780 library=Soares breast 3NBHBT vector=PT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13p1 Psitel=Not I Psite2=Eco RI Adult human 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGAGCGGCCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes, Sarcophylli; Chordata, Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 359)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, P., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 186
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 Source 1..359
 /organism="Homo sapiens"
 /clone="162780"
 BASE COUNT 83 a 113 c 80 g 78 t 5 others
 ORIGIN
 Query Match 51.6% Score 161; DB 64; Length 359;
 Best Local Similarity 87.3% Pred.No. 4.42e-272;
 Matches 220; Conservative 3; Mismatches 26; Indels 6; Gaps 4,
 Db 87 ctccaggacccctgtctgtctccagggaagagccacctctctcaggtccagtc 146
 QY 14 CTCAGCACCCCTGTCTTTCTCCAGGCAAGAGCCACCCTCTCTCTCCAGGCGCAGTC 73
 Db 147 agaatattgacacaccccttagctgtgtaccagcagagaaactggccagctccagc 206
 QY 74 AGAGTGTAAACAGT---ACTTAGCTGTGTACCAAGAAACCTGGCCAGGCTCCAGGC 130
 Db 207 tctctatctatcatcaccacaggttctcagtggtccatccagacaggttcagtingcag 266
 QY 131 TCTTCATCTATGATCATCCCAACAGAGGCACTGGCATCCAGCCAGGTTTCAGTGGCAGTG 190
 Db 267 ggtctgggacagacttttadtctcaccatncagtagactggagccctgaagattttcag 326

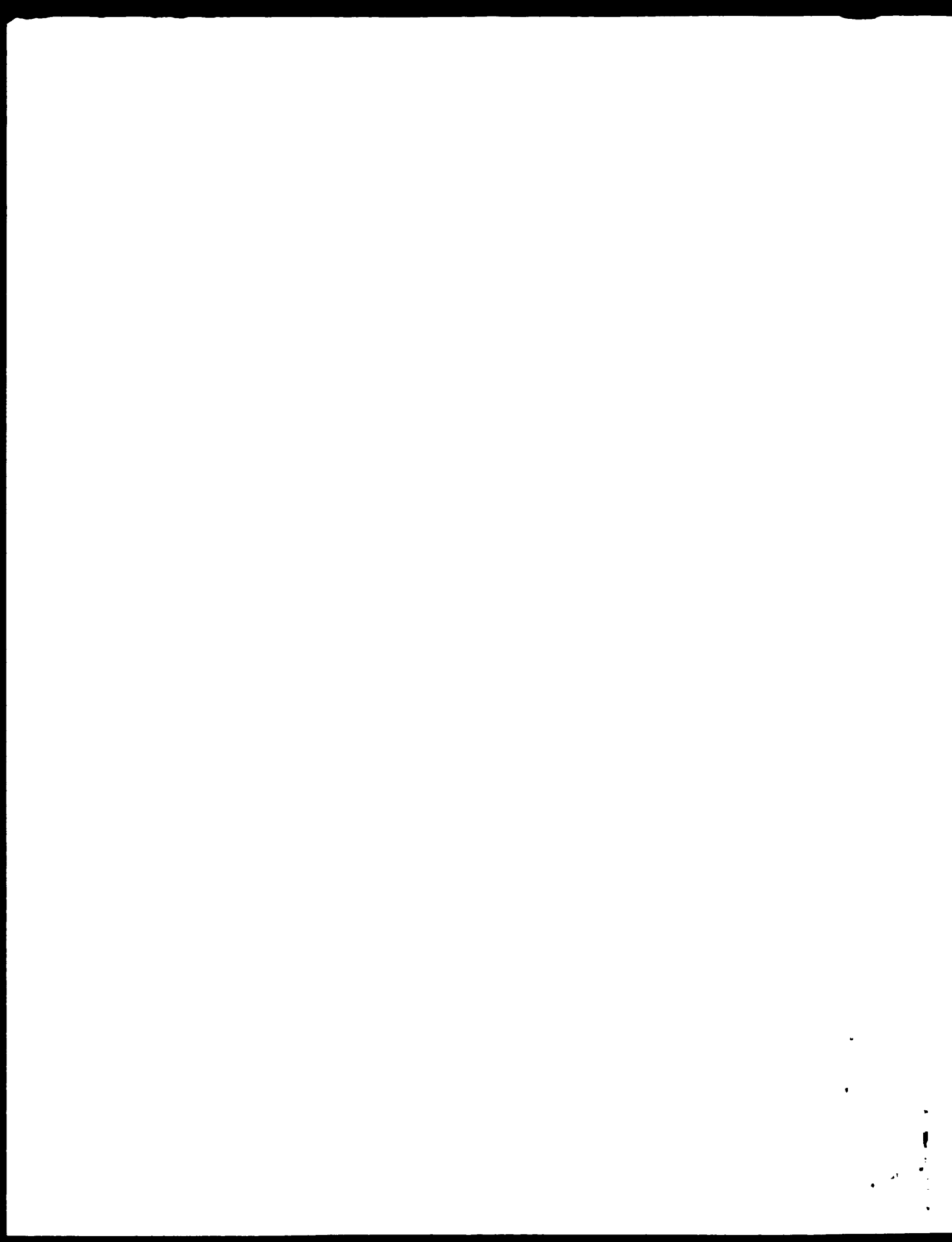
QY 191 GGTCTGGGACAGAGATTC-ACCTCTCAACCAT--CAGCAACCTAGAGGCTGAGATT 247
 Db 327 tatattactgtc 338
 QY 248 TTTATTACTGTC 259

RESULT 10
 LOCUS P10529 401 bp mRNA EST 06-APR-1995
 DEFINITION Y131906 r1 Homo sapiens cDNA clone 128434 5' similar to gb.X06764
 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
 ACCESSION R10529
 NID 9762485
 KEYWORDS EST.
 SOURCE human clone=128434 library=Soares fetal liver spleen INFIS vector=pf73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13p1 Psitel=Pac I Psite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.

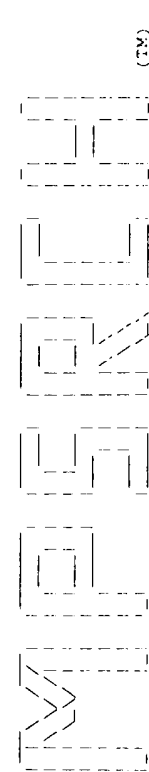
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini, Hominoidea, Homo.
 REFERENCE 1 (bases 1 to 401)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, P., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 239
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 Source 1..401
 /organism="Homo sapiens"
 /clone="128434"
 BASE COUNT 86 a 113 c 105 g 96 t 1 others
 ORIGIN
 Query Match 50.6% Score 158; DB 40; Length 401;
 Best Local Similarity 91.6% Pred.No. 8.36e-266;
 Matches 223; Conservative 0; Mismatches 11; Indels 10; Gaps 9;
 Db 74 ctccaggacccctgtctgtctccagggaagagccacctctctcaggtccagtc 133
 QY 14 CTCAGCACCCCTGTCTTTCTCCAGGCAAGAGCCACCCTCTCTCTCCAGGCGCAGTC 73
 Db 134 agaatgttagcagcagctacttagctgtgtaccagcagaaacctggccaggtccagc 193
 QY 74 AGAGTGTAAACA--AG-TACTTAGCTGTGTACCAACAGAAACCTGG--CGAGGTTCAGG 124
 Db 194 ctctctatctatgtgtcatccagcagggccactggcattccccagacagagttcagtgccag 253
 QY 130 TCTTCATCTATGATCATCCCAACAGAGGCACTGGCATCCAGCCAGGTTTCAGTGGCAGTG 188
 Db 254 tggctctgggacagacttttadtctcaccatncagtagactggagccctgaagattttt 313

[illegible]



and is derived by analysis of the total score distribution.



Release 2.10 John F. Collins, BioComputing Research Unit,
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MPsearch_nu a - a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:23:13 1998, MasPar time 410.10 seconds
Tabular output not generated
Title: >US-08-844-215-16
Description: (1-312) from US08844215 seq
Perfect Score: 312
N A Sequence: 1 GAGTTCATCTAGTCTTACG
Comp: CTCGAGTGAGTCAGAGGTCG... GGCATCAAGTTCAGATCAAA 312
CTCGAGTGAGTCAGAGGTCG... GGCATCAAGTTCAGATCTTAGTTT

Scoring table:
Gap 5
TABLE default
Nmatch STD : Dbase 0: Query 0
Searched: 430361 seqs, 710217276 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new7
1-BCT 2-PUN 3-GEN 4-HTG1 5-HTG2 6-HTG3 7-HTG4 8-HUM1
9-HUM2 10-HUM3 11-INV1 12-INV2 13-ORG 14-MAM 15-VPT
16-PLN 17-PPC1 18-PPC2 19-PPC3 20-SYN 21-UNC 22-VIP
Database: genbankal01

23-BCT1 24-BCT2 25-BCT3 26-BCT4 27-BCT5 28-BCT6 29-BCT7
30-BCT8 31-BCT9 32-BCT10 33-BCT11 34-BCT12 35-BCT13
36-GEN1 37-GEN2 38-GEN3 39-GEN4 40-GEN5 41-GEN6 42-HTG1
43-HTG2 44-HTG3 45-HTG4 46-HTG5 47-INV1 48-INV2 49-INV3
50-INV4 51-INV5 52-INV6 53-INV7 54-INV8 55-INV9 56-INV10
57-INV11 58-INV12 59-MAM1 60-MAM2 61-MAM3 62-VRT1
63-VRT2 64-VRT3 65-VRT4 66-PAT1 67-PAT2 68-PAT3 69-PAT4
70-PAT5 71-PAT6 72-PAT7 73-PHG 74-PLN1 75-PLN2 76-PLN3
77-PLN4 78-PLN5 79-PLN6 80-PLN7 81-PLN8 82-PLN9 83-PLN10
84-PLN11 85-PLN12 86-PP11 87-PP12 88-PP13 89-PP14
90-PP15 91-PP16 92-PP17 93-PP18 94-PP19 95-PP110
96-PP111 97-PP112 98-PP113 99-PP114 100-PP115 101-PP116
102-PP117 103-PP118 104-PP119 105-PP120 106-PP121 107-PP122
108-PP123 109-PP124 110-PP125 111-PP126 112-PP127 113-SYN
114-UNA
Database: genbankb101

115-VPL1 116-VPL2 117-VPL3 118-VPL4 119-VPL5 120-VPL6
121-VPL7 122-VPL8 123-VPL9 124-VPL10 125-VPL11
Database: genbank-new7
126-BCT 127-GEN 128-HTG1 129-HTG2 130-INV 131-MAM
132-VRT 133-PHG 134-PLN1 135-PLN2 136-PP11 137-PP12
138-PP13 139-SYN 140-UNA 141-VRL
Database: u-emb151_101
142-part1 143-part2

Statistics: Mean 9.943; Variance 4.455; scale 2.232
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	278	89.1	324	98	HUMHEPBBSAJ	Human hepatitis B sur	4,760,225
2	275	88.1	321	99	HUMIKCVH	Homo sapiens (clone p	3,560,224
3	274	87.8	321	93	HUMIKCVI	Homo sapiens (clone p	2,540,221
4	274	87.8	388	93	HSPOM604	H. sapiens mRNA for im	2,540,221
5	272	87.2	387	99	HUMICKVRG	Human immunoglobulin	1,970,219
6	268	85.9	381	91	HSIGVLLS	Human mRNA for LSI/VEV	1,080,215
7	266	85.3	333	91	HSAKD31G	H. sapiens rearranged	8,040,214
8	266	85.3	407	99	HUMIKKAX	Human Ig rearranged a	8,040,214
9	266	85.3	675	94	HSD03897	Human rheumatoid fact	8,040,214
10	265	84.9	384	93	HSPOM015	H. sapiens mRNA for im	6,920,213
11	264	84.6	342	93	HSSM044	H. sapiens mRNA for ka	5,950,212
12	264	84.6	345	93	HSSIP055	H. sapiens mRNA for ka	5,950,212
13	262	84.0	324	93	HUMIKKAMA	Homo sapiens anti-A m	4,150,210
14	260	81.3	294	93	HUMIKCRF	Homo sapiens (clone p	3,250,208
15	260	81.3	321	99	HUMIKCVC	Homo sapiens (clone p	3,250,208
16	260	81.3	321	99	HUMIKCVC	Homo sapiens (clone p	3,250,208
17	260	81.3	364	99	HUMAB49LG	Human mRNA for VL seq	3,250,208
18	260	81.3	297	93	HUMIKCCU	Homo sapiens (clone p	2,790,207
19	258	82.7	288	91	HSIGKV38	H. sapiens germline im	2,400,206
20	258	82.7	294	91	HSIGKV023	Human rearranged immu	2,400,206
21	258	82.7	321	93	HUMIKCVA	Homo sapiens (clone p	2,400,204
22	258	82.7	322	99	HUMIKCVD	Homo sapiens (clone p	2,400,204
23	258	82.7	324	99	HUMIKCVD	Homo sapiens (clone p	2,400,204
24	258	82.7	345	93	HSSIP015	H. sapiens mRNA for ka	2,400,204
25	258	82.7	345	93	HSSIP026	H. sapiens mRNA for ka	2,400,204
26	258	82.7	364	99	HUMAB13LC	Human mRNA for VL seq	2,400,204
27	258	82.7	384	91	HSIGKLV68	H. sapiens mRNA for re	2,400,204
28	258	82.7	797	91	HSIGKLC1	Human germline frame	2,400,204
29	257	82.4	376	91	HSIGKLV33	H. sapiens mRNA for re	2,400,204
30	257	82.4	384	93	HSPOM023	H. sapiens mRNA for re	2,400,204
31	256	82.1	345	93	HSSIP042	H. sapiens mRNA for ka	1,770,204
32	256	82.1	345	93	HSSIP006	H. sapiens mRNA for ka	1,770,204
33	256	82.1	345	93	HSSIP017	H. sapiens mRNA for ka	1,770,204
34	256	82.1	387	93	HSPOM031	H. sapiens mRNA for im	1,770,204
35	256	82.1	797	99	HUMIKCVD	Human Ig germline kuf	1,770,204
36	254	81.4	321	93	HSPMVL1G	H. sapiens mRNA for re	1,300,202
37	254	81.4	323	99	HUMIKLRFH	Homo sapiens (HOLL) f	1,300,202
38	254	81.4	327	92	HSLVL1	H. sapiens mRNA for re	1,300,202
39	254	81.4	333	95	HSP0772	Human anti-HIV-1 p21	1,260,202
40	254	81.4	345	93	HSSIP011	H. sapiens mRNA for ka	1,300,202
41	254	81.4	345	93	HSSIP021	H. sapiens mRNA for ka	1,300,202
42	254	81.4	345	93	HSSIP022	H. sapiens mRNA for ka	1,300,202
43	254	81.4	345	93	HSSIP059	H. sapiens mRNA for ka	1,300,202
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45	254	81.4	345	93	HSSIP003	H. sapiens mRNA for ka	1,300,202

ALIGNMENTS

RESULT 1 HUMHEPBBSAJ 324 bp mRNA PRI 17 JUN 1992
LOCUS Human hepatitis B surface antigen antibody variable domain mRNA,
DEFINITION partial cds.
ACCESSION M83317
KEYWORDS antibody variable domain; hepatitis B surface antigen antibody.
SOURCE Homo sapiens (individual isolate CM, library, JMI4, blood DNA to
ORGANISM Homo sapiens
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 324)
DeGraw, J., Pyatt, J., Lapolla, P., Burton, D.R., Lerner, R.A. and
Thornton, G.B.
TITLE Human combinatorial antibody libraries to hepatitis B surface

JOURNAL Proc Natl Acad Sci U S A 89, 3175-3179 (1992)
 MEDLINE 92228746
 FEATURES
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 Location/Qualifiers
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 BASE COUNT 73 a 100 c 83 g 68 t
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 Db 64 tgcagggccagtcagagtggttagcagcttaettagctcctggtgtaccacagaaacccctggccag 123
 QY 1 GCTCCAGGCTCTCTCATATGATGATGATCAACAGGGGCTCATGTGCATCCCCAGCCAGGCTTC 180
 Db 184 agtggcagtggtgtctgggacagacttcaactctcaccatcagcagcctagagcctgaagat 243
 QY 181 AGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGCCTGAAGAT 240
 Db 244 ttgcagtttattactgtccagcagctagcagctgagcactggcctctcttcttgcggcaggagacc 303
 QY 241 TTTCAGGTTTATTACTGTACAGCGGTAGCCACTGGG-TCA--CTTTCGGCGGAGGAGCC 297
 Db 304 aaggtggagatcaaa 318
 QY 298 AAGGTGGAGATCAAA 312

RESULT 2 HUMIKCVH 321 bp mRNA PRI 02-MAY-1996
 LOCUS Homo sapiens (clone pAG21) Ig kappa chain mRNA, V-region, partial cds.
 DEFINITION
 ACCESSION L37308
 NID g845531
 KEYWORDS immunoglobulin light chain; kappa-immunoglobulin; variable region.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 321)
 REFERENCE Chlin.M., Sundqvist,V.A., Mach,M., Wahren,B. and Borrebaeck,C.A.
 AUTHORS Fine specificity of the human immune response to the major
 TITLE neutralization epitopes expressed on cytomegalovirus gp58/116 (gB),
 as determined with human monoclonal antibodies
 J. Virol. 67 (2), 703-710 (1993)
 JOURNAL 93124562
 MEDLINE
 REFERENCE 2 (bases 1 to 321)
 AUTHORS Chlin.M., Gwan.H., Mach,M. and Borrebaeck,C.A.
 TITLE Light chain shuffling of a high affinity antibody results in a
 drift in epitope recognition
 JOURNAL Mol. Immunol. 33 (1), 47-56 (1996)
 MEDLINE 96174997

Location/Qualifiers
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 /clone="pAG21"
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 BASE COUNT 75 a 98 c 81 g 67 t
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 Db 68 gcagggccagtcagagtggttagcagcttaettagctcctggtgtaccacagaaacccctggcagg 127
 QY 62 GCAGGGCCAGTCAGAGTGTTCACAGTACTTAGCCCTGGTACCAACAGAAACCTGGCCAGG 121
 Db 128 ctcccagctctcctcatctatgatgcatacacaagagccactggcctcaccagcagattca 187
 QY 122 CTCGCCAGGCTCTCTCATCTATGATGATGATCAACAGGGGCTCATGTGATCATAGAGTTCA 181
 Db 188 gtggcagtggtgtctgggacagacttcaactctcaccatcagcagcctagagcctgaagatt 247
 QY 182 GTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGCCTGAAGATT 241
 Db 248 ttgcagtttattactgtccagcagctagcagcactggcctcctcacttctcggcaggagacca 307
 QY 242 TTGCAGTTTATTACTGTACAGCGGTAGCCACTGGG---TCACTTTCGGCGGAGGAGCA 298
 Db 308 aggtggagatcaaa 321
 QY 299 AGGTGGAGATCAAA 312

RESULT 3 HUMIKCVI 321 bp mRNA PRI 02-MAY-1996
 LOCUS Homo sapiens (clone pAG21B) Ig kappa chain mRNA, V-region, partial cds.
 DEFINITION
 ACCESSION L37309
 NID g845533
 KEYWORDS immunoglobulin light chain; kappa-immunoglobulin; variable region.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 321)
 REFERENCE Chlin.M., Sundqvist,V.A., Mach,M., Wahren,B. and Borrebaeck,C.A.
 AUTHORS Fine specificity of the human immune response to the major
 TITLE neutralization epitopes expressed on cytomegalovirus gp58/116 (gB),
 as determined with human monoclonal antibodies
 J. Virol. 67 (2), 703-710 (1993)
 JOURNAL


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Matches 295; Conservative 0; Mismatches 11; Indels 3; Gaps 2;

Db 13 acacagctccacgacacccctgtctttgtctccaggggaagagagacacacctctctctacag 72
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Db 73 gccagtcagaggttagcagctactagcctggttacacacagaaacctggccaggctccc 132
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Db 193 agtggatctggacagagacttcacttcaccatccagcagccttagagcctgaagattttaga 252
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Qy 187 AGTGGGTCTGGACAGACTTCACTCTACCATCAGCAACCTAGAGCTGAAGATTTTTGA 246

Db 253 gttttattactgtcagcagcctagcaacttgcgcgttgagccttgcgcgaaggacccaaggttt 312
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QY	304	GAGATCAAA	312
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DEFINITION		Human Ig rearranged anti-myelin kappa-chain mRNA V-J4-region, hybridoma AE6-5, 5' end.	04-JAN-1995 PBI
ACCESSION		M29469	
NID		5185922	
KEYWORDS		J-region, V-region, autoantibody, immunoglobulin kappa processed gene; variable region subgroup VK-IIIA.	
SOURCE		Human (patient PBP) hybridoma AE6-5 DNA, clone PBP-PVK, derived from B-CLL cell line Hc724-6.	
ORGANISM		Homo sapiens	
PEREQUENCE		Eukaryotes; mitochondrial leukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS		Spatz, L.A., Wong, K.K., Williams, M., Desai, R., Golier, J., Berman, E., Alt, F.W. and Latov, N.	
TITLE		Cloning and sequence analysis of the VH and VL regions of an anti-myelin/DNA antibody from a patient with peripheral neuropathy and chronic lymphocytic leukemia	
JOURNAL		J. Immunol. 144 (7), 2621-2624 (1990)	
MEDLINE		92030363	
COMMENT		Draft entry and printed sequence for [1] kindly submitted by L.A. Spatz, 26-OCT-1989, for release after publication. Columbia University, Department of Neurology EB-322, 630 W. 168th street, New York, NY 10032.	
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Db 156 gccactcagagttagcaactttagccttagcttagtaccacacacacacacacacaccc 215
Qy 67 GCCAGTCAGAGTGTATCAAGTACTTAGCCTGTGTACCAACAGAAACCTTGGCCAGGCTCCC 126
Db 215 aggcctctctctatgatgcacacacacacacacacacacacacacacacacacacaccc 275
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Db 396 gagatcaaa 404
Qy 304 GAGATCAAA 312

RESULT 9      HSU03897      675 bp      DNA      PRI      02-AUG-1994
LOCUS      Human rheumatoid factor D1 IgG light chain VK3 region rearranged
DEFINITION      (humka3d1) gene, partial cds.
ACCESSION      U03897
NID      9485725
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE      1 (bases 1 to 627)
AUTHORS      Deftos, M., Olee, T., Carson, D.A. and Chen, P.P.
TITLE      Defining the genetic origins of three rheumatoid synovium-derived
JOURNAL      IgG rheumatoid factors
MEDLINE      J. Clin. Invest. 93 (5), 2545-2553 (1994)
REFERENCE      2 (bases 1 to 675)
AUTHORS      Chen, P.P.
TITLE      Direct Submission
JOURNAL      Submitted (01-DEC-1993) Popen V. Chen, Medicine, University of
California San Diego, 9500 Gilman Dr., La Jolla, CA 92037-0663, USA
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Matches 295; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
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Qy 187 AGTGSGTCTGGGACAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 246
Db 595 gtttattactgtcagcagcagtagcaagtgcctctcactcttcggtcggcggagggacacaggtg 654
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Db 655 gaaatcaaa 663
Qy 304 GAGATCAAA 312

RESULT 10     HSPOM015     384 bp      DNA      PRI      02-JUN-1996
LOCUS      H sapiens mRNA for immunoglobulin kappa light chain VJ region (H
DEFINITION      POM015).
ACCESSION      Z689901
NID      g1359843
KEYWORDS      immunoglobulin; immunoglobulin kappa chain; immunoglobulin light
SOURCE      chain; joining region; variable region.
ORGANISM      human.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE      1 (bases 1 to 384)
AUTHORS      Juul, L., Hougs, L., Andersen, V., Sveigaard, A. and Parington, I.
TITLE      The normally expressed kappa immunoglobulin light chain gene
reertoire. Frequent occurrence of features often assigned to
autoimmunity
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 384)
AUTHORS      Juul, L.
TITLE      Direct Submission
JOURNAL      Submitted (22-JAN-1996) Juul L., Dept. of Clinical Immunology KI
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
2200 Copenhagen N, DENMARK

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11

WIREH

(TM)

Release 2.1D John F. Collins, Bioinformatics Research Unit.
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MPSrch_nu n a - n a database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 13:56:38 1998. MaxPar time 19.34 seconds
Tabular output not generated. 742.038 Million cell updates/sec

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Comp: CTCGAGTGAGTACAGAGGTCG.....CTGGGTCCAGCTCAGTTT

Scoring table: TABLE default
Gap 6

Mismatch STD : Dbase 0; Query 0

Searched: 87531 seqs, 22996021 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1-back1 2 51 3 52 5 54 5 55 7 56 8 PCT90 9 PCT91
10-PCT92 11-PCT93 12-PCT94 13-PCT95 14-PCT96

Statistics: Mean 7.621; Variance 4.215; scale 1.808

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				Pred No	
Result No.	Score	Match	Length	Description	
1	258	82.7	812	US-08-053- Sequence 178, Applicat	1.76e-173
2	252	80.8	900	US-08-053- Sequence 180, Applicat	6.69e-164
3	228	73.1	646	PCT-US95-1 Sequence 2, Applicatio	1.30e-150
4	228	73.1	646	PCT-US94-0 Sequence 2, Applicatio	1.30e-150
5	228	73.1	646	US-08-300- Sequence 2, Applicatio	1.30e-150
6	218	69.9	900	US-08-053- Sequence 182, Applicat	5.32e-143
7	206	66.0	325	PCT-US93-1 Sequence 1, Applicatio	6.70e-134
8	162	51.9	729	US-08-376- Sequence 152, Applicat	1.10e-100
9	162	51.9	729	PCT-US95-0 Sequence 152, Applicat	1.10e-100
10	162	51.9	729	PCT-US95-0 Sequence 153, Applicat	1.10e-100
11	162	51.9	729	US-08-376- Sequence 154, Applicat	1.10e-100
12	162	51.9	13254	US-08-376- Sequence 155, Applicat	1.10e-100
13	162	51.9	13254	PCT-US95-0 Sequence 156, Applicat	1.10e-100
14	162	51.9	13254	PCT-US95-0 Sequence 157, Applicat	1.10e-100
15	162	51.9	13254	US-08-376- Sequence 158, Applicat	1.10e-100
16	142	45.5	5238	1 5453363-1 Patent No. 5453363	1.04e-85
17	140	44.9	381	US-08-477- Sequence 82, Applicat	3.23e-84
18	140	44.9	381	US-08-487- Sequence 82, Applicat	3.23e-84
19	140	44.9	381	US-07-634- Sequence 82, Applicat	3.23e-84

20 140 44.9 321 7 US-08-474- Sequence 82, Applicat 3.23e-84
21 139 44.6 280 12 PCT-US95-1 Sequence 82, Applicat 1.80e-83
22 139 44.6 280 7 US-08-400- Sequence 1, Applicatio 1.80e-83
23 137 43.9 387 6 US-08-217- Sequence 184, Applicat 5.56e-82
24 137 43.9 387 7 US-08-053- Sequence 12, Applicat 5.56e-82
25 133 42.6 384 7 US-08-458- Sequence 13, Applicat 5.27e-79
26 133 42.6 384 6 US-08-259- Sequence 3, Applicatio 1.62e-77
27 131 42.0 599 6 US-08-339- Sequence 72, Applicat 1.62e-77
28 129 41.3 321 7 US-08-425- Sequence 74, Applicat 1.62e-77
29 129 41.3 321 10 PCT-US92-0 Sequence 74, Applicat 1.62e-77
30 129 41.3 321 5 US-07-988- Sequence 89, Applicat 1.62e-77
31 129 41.3 723 5 US-08-425- Sequence 92, Applicat 1.62e-77
32 129 41.3 723 5 US-07-988- Sequence 92, Applicat 1.62e-77
33 129 41.3 723 7 US-08-455- Sequence 93, Applicat 1.62e-77
34 129 41.3 723 5 US-07-988- Sequence 93, Applicat 1.62e-77
35 129 41.3 723 10 PCT-US92-0 Sequence 92, Applicat 1.62e-77
36 129 41.3 723 10 PCT-US92-0 Sequence 92, Applicat 1.62e-77
37 127 40.7 321 5 US-08-208- Sequence 2, Applicatio 1.51e-74
38 125 40.1 483 13 PCT-US95-0 Sequence 14, Applicat 1.51e-74
39 125 40.1 483 13 PCT-US95-0 Sequence 1, Applicatio 1.51e-74
40 124 39.7 1238 7 US-08-401- Sequence 35, Applicat 2.52e-72
41 124 39.7 1300 7 US-08-401- Sequence 34, Applicat 2.52e-72
42 123 39.4 318 12 PCT-US94-1 Sequence 2, Applicatio 1.39e-71
43 123 39.4 318 11 PCT-US93-0 Sequence 3, Applicatio 1.39e-71
44 123 39.4 318 11 PCT-US93-0 Sequence 3, Applicatio 1.39e-71
45 123 39.4 321 7 US-08-425- Sequence 69, Applicat 1.39e-71

ALIGNMENTS

RESULT 1
ID US-08-053-131-178 STANDARD; DNA; UNC; 812 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 178, Application US/08053131.
CC Sequence 178, Application US/08053131
CC Patent No. 5661016
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antipodios
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patented Release #1.0. Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053/131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/000,860
CC FILING DATE: 15-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/950,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO. 178:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 812 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: Join(199, 246, 418, 714)
CC Sequence 812 bp: 253 A; 255 C; 187 G; 199 T; 0 other;
Query Match 82.7%; Score 258; DB 7; Length 812;
Best Local Similarity 97.8%; Pred. No. 1.76e-173;
Matches 264; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db 442 ACACAGCTCCAGCCAGCTGCTTTGTCTCCAGGGGAAAGAGCCCTCTCTCTGCGAG 501
QY 7 ACTCAGTCTCCAGCCAGCTGCTTTGTCTCCAGGGGAAAGAGCCCTCTCTCTGCGAG 56
Db 502 GCCAGTCAGAGTGTATAGAGTACTTAGCTGTGTATACCAAGAAAGCTGTGCGAGCTCC 561
QY 67 GCCAGTCAGAGTGTATACAGTACTTAGCTGTGTATACCAAGAAAGCTGTGCGAGCTCC 126
Db 562 AGGTCCTCATCTATATGATGATACCAAGAGGCTATGCTATGCTATGCTATGCTATGCT 621
QY 127 AGGTCCTCATCTATGATGATACCAAGAGGCTATGCTATGCTATGCTATGCTATGCT 186
Db 622 AGTGGTCTCGGACAGCTTCACTCTCACCATCAGCAGCTAGAGCTTGAAGATTTTGA 681
QY 187 AGTGGTCTCGGACAGCTTCACTCTCACCATCAGCAGCTAGAGCTTGAAGATTTTGA 246
Db 682 GTTATTACTGTCCAGCGCTAGCAACTGG 711
QY 247 GTTATTACTGTCCAGCGCTAGCGACTGG 276
RESULT 2
ID US-08-053-131-180 STANDARD: DNA: UNC: 900 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 180, Application US/08053131.
CC Sequence 180, Application US/08053131
CC Patent No. 5661016
CC GENERAL INFORMATION:
CC APPLICANT: Lomborg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Hourie and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/810,279

CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 180:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 900 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: Join(180, 227, 397, 693)
CC Sequence 900 bp: 225 A; 244 C; 204 G; 227 T; 0 other;
Query Match 80.8%; Score 252; DB 7; Length 900;
Best Local Similarity 96.7%; Pred. No. 6.69e-169;
Matches 261; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 421 ACACAGCTCCAGCCAGCTGCTTTGTCTCCAGGGGAAAGAGCCCTCTCTCTGCGAG 480
QY 7 ACTCAGTCTCCAGCCAGCTGCTTTGTCTCCAGGGGAAAGAGCCCTCTCTCTGCGAG 66
Db 481 GCCAGTCAGGCTGTAGCAGCTACTTAGCTGTGTATACCAAGTACTTAGCTGTGTATACCA 540
QY 67 GCCAGTCAGGCTGTAAACAAGTACTTAGCTGTGTATACCAAGTACTTAGCTGTGTATACCA 126
Db 541 AGGTCCTCATCTATGATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 600
QY 127 AGGTCCTCATCTATGATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 186
Db 601 AGTGGTCTCGGACAGCTTCACTCTCACCATCAGCAGCTAGAGCTTGAAGATTTTGA 550
QY 187 AGTGGTCTCGGACAGCTTCACTCTCACCATCAGCAGCTAGAGCTTGAAGATTTTGA 246
Db 661 GTTATTACTGTCCAGCGCTAGCAACTGG 690
QY 247 GTTATTACTGTCCAGCGCTAGCGACTGG 276
RESULT 3
ID PCT-US95-11235-2 STANDARD: DNA: UNC: 646 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 2, Application PC/TUS9511235.
CC Sequence 2, Application PC/TUS9511235.
CC GENERAL INFORMATION:
CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
CC TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
CC TITLE OF INVENTION: USING UNIVERSAL OR PANI-MIZED IMMUNOCLONAL IN LIGHT
CHAINS
CC NUMBER OF SEQUENCES: 70
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute
CC STREET: 10555 North Torrey Pines Road, TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US 07/810,279

CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute
 CC STREET: 10555 No 564798th Torrey Pines Road, TPCR
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/400,386A
 CC FILING DATE: 02-SEP-1994
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/174,674
 CC FILING DATE: 28-DEC-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/826,623
 CC FILING DATE: 27-JAN-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/012,566
 CC FILING DATE: 02-FEB-1993
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: TSP1 409.1
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO. 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 646 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: cDNA
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC Sequence 646 bp; 162 A, 187 C, 170 G, 127 T, 0 other;

Query Match 73.1% Score 228; DB 7; Length 646;
 Best Local Similarity 88.6%; Pred No 1 100-100,
 Matches 279; Conservative 0; Mismatches 33; Indels 3; Gaps 1;
 Db 1 GAGCTCAGGAGCTCTCCAGGAGCCCTGTCTTTGTCTCCAGGGGAAAGAGGACGACCTCTCC 60
 QY 1 GAGCTCAGGAGCTCTCCAGGAGCCCTGTCTTTGTCTCCAGGGGAAAGAGGAGGACGACCTCTCC 60
 Db 61 TCGAGGGGAGGAGCTCAAGTCTTTAAGAGGAGTACTAGGCTGTGTACAGAGAGAAAGGAGGAGG 120
 QY 61 TCGAGGGGAGGAGCTCAAGTCTTTAAGAGGAGTACTAGGCTGTGTACAGAGAGAAAGGAGGAGG 117
 Db 121 CAGGCTCCAGGAGCTCTCTATCTATCTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 180
 QY 118 CAGGCTCCAGGAGCTCTCTATCTATCTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 177
 Db 181 TCGAGTGGGAGGAGTGGTCTGGGAGAGAGCTTCACTCTCAGCATCAGAGAGCTGGAGGCTGAA 240
 QY 178 TCGAGTGGGAGGAGTGGTCTGGGAGAGAGCTTCACTCTCAGCATCAGAGAGCTGGAGGCTGAA 237
 Db 241 GATTCTTGCAGTGTACTATCTATCTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 300
 QY 238 GATTCTTGCAGTGTACTATCTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 297
 Db 301 AAGTGGGAATCAAA 315
 QY 298 AAGTGGGAGATCAAA 312

RESULT 6
 ID US-08-053-131-182 STANDARD; DNA; UNC; 900 BP.
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 182, Application US/08053131.
 CC Sequence 182, Application US/08053131
 CC Patent No. 5661016
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic No 5661016-Human Animals for
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 197
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: One Market Plaza, Stewart Tower, Suite 200
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/053,131
 CC FILING DATE: 26-APR-1993
 CC CLASSIFICATION: 800
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/990,860
 CC FILING DATE: 16-DEC-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/810,279
 CC FILING DATE: 17-DEC-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/853,408
 CC FILING DATE: 18-MAR-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-9-3
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO. 182:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 900 base pairs
 CC TYPE: nucleic acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: DNA (genomic)
 CC FEATURE:
 CC NAME/KEY: CDS
 CC LOCATION: join(116..163, 351..650)
 CC Sequence 900 BP; 220 A; 241 C; 201 G; 238 T; 0 other;
 Query Match 69.9% Score 218; DB 7; Length 900;
 Best Local Similarity 94.6%; Pred No 5 22e-143;
 Matches 247; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
 Db 375 AGGAGTGTCCAGGAGCCCTGTCTTTGTCTCCAGGGGAAAGAGGAGGAGGAGGAGGAGGAGG 434
 QY 7 ACTCAGTCTCCAGGAGCCCTGTCTTTGTCTCCAGGGGAAAGAGGAGGAGGAGGAGGAGGAGG 66
 Db 435 GCCAGTGTAGAGTGTGTAGCAGCAGCTACTAGCTGTGTAGCTGTGTAGCTGTGTAGCTGTGTAG 494
 QY 67 GCCAGTGTAGAGTGTGTAGCAGCAGCTACTAGCTGTGTAGCTGTGTAGCTGTGTAGCTGTGTAG 123
 Db 455 GCCAGGAGTGTGTATGT 554


```

CC APPLICANT: Letner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10566 N. Torrey Pines Road, Suite 220,
CC STREET: Mail Drop IPW
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER PEACABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SRI1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 168:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 729 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SQ Sequence 729 BP: 155 A 192 G 208 G 173 T 0 other:
Query Match 51.9% Score 142 DB 7 Length 729:
Best Local Similarity 53.9% Pred No. 110e-100:
Matches 219 Conservative 0 Mismatches 19 Gaps
Ddb 392 CTGACATATAGTGTAAATCTTTTCAGAGTGCTACTCTGGTATGATGAGATGAAGTC 451
Ccp 251 CTGACATATAAAGCTCAAAAATCTTCAGAGTGCTACTCTGGTATGATGAGATGAAGTC 202
Ddb 452 TGTCGCAGAGCGGCTGCTTAAGTCTTTGATATGTCAGAGGCTCTATTGCAAAACAG 511
Ccp 201 TATTTGATAGGCTGCTGATATGAGCTTGGTATGCTATGATGATGATGATGATGAT 142
Ddb 512 ATGTATGATAGGCTTGTGATTTGGGTCAGATTTGTGTGGTAGACAGAGCTACAGGAGG 691
Ccp 141 ATATATGAGGAGAGCTGGAGAGCTGGGTCAGATTTGTGTGGTAGACAGAGCTAACG 95
Ddb 572 CGCAATGCTGTATGAGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
Ccp 84 GTTAATATGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 26
Ddb 612 GGTGCTGGGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 652
Ccp 24 GTTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4

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[illegible]

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RESULT 13
ID PCT-US95-08743-156 STANDARD; DNA: UNC: 13254 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 156, Application PC/TUS9508743.
CC Sequence 156, Application PC/TUS9508743.
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 13254 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: circular
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 13254 BP; 3238 A; 3251 C; 3559 G; 3206 T; 0 other:
SQ
Query Match 51.9%; Score 162; DB 13; Length 13254;
Best Local Similarity 83.9%; Pred. No. 1.10e-100;
Matches 219; Conservative 0; Mismatches 39; Indels 3; Gaps 2;

Db 389 CTCACAGTAGTACAGTGCAGAACTTTTCAGGCTCCACTCTGCTGATGAGTGAAGTC 448
Cp 261 CTCACAGTAGTAAATATGCAAAATCTTCAGGCTCTAGGTTGTGATGCTGATGAGTGAAGTC 202
Db 449 TGTCCAGACATCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 508
Cp 201 TGTCCAGACATCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 142
Db 509 ATGTATGACGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 568
Cp 141 ATAGATGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 85
Db 569 GCGAATGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 628
Cp 84 GTTACACATCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 25
Db 629 GGTGCTGGAGACTGCGTGAG 649
Cp 24 GGTGCTGGAGACTGAGTGAG 4

RESULT 15
ID US-08-276-852-170 STANDARD; DNA: UNC: 13254 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 170, Application US/08276852
CC Sequence 170, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis P
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESS: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514

Db 12605 CTCACGAGTCTCCAGCAGCTGCTCTGCTCCAGGGAAGAGAGGAGCTCTCTCTGT 12665
Cp 4 CTCACGAGTCTCCAGCAGCTGCTCTGCTCTCCAGGGAAGAGAGGAGCTCTCTCTGTCTCTCTGC 63
Db 12666 AGGTCCAGTCCAGCAGCTTCCAGCAGCTGCTCTGCTCCAGCAGCAGCAGCAGCAGCAGCAGCAG 12725
Cp 64 AGGCTCCAGTCCAGCAGCTTCCAGCAGCTGCTCTGCTCCAGCAGCAGCAGCAGCAGCAGCAGCAG 120
Db 12726 GCTCCAGGCTGCTCAGATGCTCTTTCATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12785
Cp 121 GCTCCAGGCTGCTCAGATGCTCTTTCATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 12786 AGGCTCCAGTCCAGCAGCTTCCAGCAGCTGCTCTGCTCCAGCAGCAGCAGCAGCAGCAGCAGCAG 12845
Cp 181 AGTGGCAGTGGCTGGAGCAGACTTCTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
Db 12846 TTGCACTGTAAGTCTGCTGAG 12866
Cp 241 TTGCACTGTAAGTCTGCTGAG 261

RESULT 14
ID PCT-US95-08743-170 STANDARD; DNA: UNC: 13254 BP
AC xxxxxx
DT 01-JAN-1900
DE Sequence 170, Application PC/TUS9508743.
CC Sequence 170, Application PC/TUS9508743.
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
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CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SP91452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 170:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 13254 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: circular
CC MOLECULE TYPE: DNA (genomic)
CC Sequence 13254 BP: 3238 A; 3251 C; 3559 G; 3206 T; 0 other;

Query Match 51.9%; Score 162; DB 7; Length 13254;
Best Local Similarity 83.9%; Pred. No. 1.10e-100;
Matches 219, Conservative 0, Mismatches 39, Indels 3, Gaps 2,

Db 389 CTGACAGTACTGACAGTGCAGAGCTTCAGGCTCCACTCTGTGTGATGGTGAGAGTGAAGTC 448
Cp 261 CTGACAGTAAATAATGTCAGAAATCTTAAAGCTCTAGGTTGCTGATGGTGAGAGTGAAGTC 202
Db 449 TGTCGACAGACCCACTGCTGCTGAACTCTCTGAGATGACAGAGGACCTATTGGAAACACC 508
Cp 201 TGTCGACAGACCCACTGCTGCTGAACTCTCTGAGATGACAGAGGACCTATTGGATGCATC 142
Db 509 ATGTATGACAGACCTTTGGAGAGCTGGCCAGGTTTGTGCTGGTACAGAGGCTACGCGGCGGCT 568
Cp 141 ATAGATGAGAGAGCTGGGAGAGCTGGCCAGGTTTGTGCTGGTACAGAGGCTACGCGGCGGCT 85
Db 569 GCGAATGCTGTGACTGGACCTACAGAGAGAGGAGGCTCTTTCCCGCTGGAGACAGAGACAG 628
Cp 84 GTTACACTCTGACTGGCCCTGACAGAGAGGAGGCTCTTTCCCGCTGGAGACAGAGACAG 25
Db 629 GTGCGCTGGAGACTGCGTGAG 649
Cp 24 GTTGGCTGGAGACTGAGTGAG 4

Search completed: Tue Feb 24 13:57:30 1998
Job time : 52 secs.

13

WATERMAN

(TM)

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Distribution rights by IntelliGenetics, Inc.

MPsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm
Run On: Tue Feb 24 07 19 58 1998. MasPar time 112.36 Seconds
Tabular output not generated.

Title: >US-08-844-215-15
Description: (1-318) from US08844215.seq
Perfect Score: 318
N.A. Sequence: 1 GAGCTACGAGCTCTCCAGG
N.A. Comp: CTCGAGTGGCTCAGAGTCC... GTCGCTTCACCTCTAGTTT

Scoring table:
Gap 6
TABLE default

Nmatch STD : Dbase 0: Query 0

Searched: 332433 seqs, 126143548 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:
1-STS1 2-STS2 3-STS3 4-STS4 5-STS5 6-STS6 7-STS7 8-STS8
9-STS9 10-STS10 11-STS11 12-STS12 13-STS13 14-STS14
15-STS15 16-STS16 17-STS17 18-STS18 19-STS19
20-STS20 21-STS21 22-STS22 23-STS23 24-STS24
25-STS25 26-STS26 27-STS27 28-STS28 29-STS29
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45-STS45 46-STS46 47-STS47 48-STS48 49-STS49
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85-STS85 86-STS86 87-STS87 88-STS88 89-STS89
90-STS90 91-STS91 92-STS92 93-STS93 94-STS94
95-STS95 96-STS96

Statistics: Mean 9.875: Variance 2.009: scale 4.916

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match length	ID	Description	Pred. No.
1	272	85.5	400.50	HS1244850	272761 r1 Soares cva 0.00e-00
2	229	75.2	418.39	AA512339	272761 r1 Soares cva 0.00e-00

3	239	75.2	418.71	HS1308977	272761 r1 Soares cva 0.00e-00
4	207	65.1	242.64	HS1368312	272761 r1 Soares cva 0.00e-00
5	207	65.1	242.64	AA472857	272761 r1 Soares cva 0.00e-00
6	165	51.9	240.59	HS1326090	272761 r1 Soares cva 1.80e-264
7	158	49.7	171.25	AA475303	272761 r1 Soares cva 1.27e-255
8	158	49.7	171.25	HS1326793	272761 r1 Soares cva 1.27e-255
9	156	49.1	324.63	AA454234	272761 r1 Soares cva 4.34e-251
10	156	49.1	324.63	HS1358064	272761 r1 Soares cva 4.34e-251
11	151	47.5	217.38	AA440059	272761 r1 Soares cva 1.36e-241
12	151	47.5	217.38	HS1324569	272761 r1 Soares cva 1.36e-241
13	137	43.1	260.49	HS1145381	272761 r1 Soares cva 3.33e-214
14	137	43.1	260.49	AA452131	272761 r1 Soares cva 3.33e-214
15	134	42.1	262.38	AA452131	272761 r1 Soares cva 3.33e-214
16	134	42.1	262.38	HS1320157	272761 r1 Soares cva 3.33e-214
17	132	41.5	240.55	HS1320157	272761 r1 Soares cva 3.33e-214
18	132	41.5	240.55	AA454451	272761 r1 Soares cva 3.33e-214
19	130	40.9	243.52	AA454451	272761 r1 Soares cva 3.33e-214
20	130	40.9	243.52	HS1320157	272761 r1 Soares cva 3.33e-214
21	130	40.9	243.52	AA454451	272761 r1 Soares cva 3.33e-214
22	128	40.3	244.57	HS1320157	272761 r1 Soares cva 3.33e-214
23	128	40.3	244.57	AA454451	272761 r1 Soares cva 3.33e-214
24	126	39.6	242.64	HS1320157	272761 r1 Soares cva 3.33e-214
25	126	39.6	242.64	AA454451	272761 r1 Soares cva 3.33e-214
26	124	39.0	242.64	HS1320157	272761 r1 Soares cva 3.33e-214
27	124	39.0	242.64	AA454451	272761 r1 Soares cva 3.33e-214
28	124	39.0	242.64	HS1320157	272761 r1 Soares cva 3.33e-214
29	120	37.4	240.54	HS1320157	272761 r1 Soares cva 3.33e-214
30	119	37.4	240.54	AA454451	272761 r1 Soares cva 3.33e-214
31	119	37.4	240.54	HS1320157	272761 r1 Soares cva 3.33e-214
32	108	34.0	239.50	AA454451	272761 r1 Soares cva 3.33e-214
33	108	34.0	239.50	HS1320157	272761 r1 Soares cva 3.33e-214
34	97	30.5	442.78	HS1320157	272761 r1 Soares cva 3.33e-214
35	95	29.9	240.55	AA454451	272761 r1 Soares cva 3.33e-214
36	95	29.9	240.55	HS1320157	272761 r1 Soares cva 3.33e-214
37	94	29.6	363.10	AA454451	272761 r1 Soares cva 3.33e-214
38	94	29.6	363.10	HS1320157	272761 r1 Soares cva 3.33e-214
39	91	28.5	242.64	AA454451	272761 r1 Soares cva 3.33e-214
40	91	28.5	242.64	HS1320157	272761 r1 Soares cva 3.33e-214
41	90	28.3	287.33	AA454451	272761 r1 Soares cva 3.33e-214
42	90	28.3	287.33	HS1320157	272761 r1 Soares cva 3.33e-214
43	66	20.8	335.54	HS1320157	272761 r1 Soares cva 3.33e-214
44	63	19.8	139.64	HS1320157	272761 r1 Soares cva 3.33e-214
45	63	19.8	139.64	AA454451	272761 r1 Soares cva 3.33e-214

ALIGNMENTS

RESULT 1
ID HS1244850 standard: RNA, EST: 400 BP.

AC AA456778;
NI 92177199
DT 07-JUN-1997 (Pel. 52, Created)
DE 272761 r1 Soares cva; tumor NHEKt Homo sapiens cDNA clone 770541
DE 5: similar to gb:X05764 F5 KAPPA CHAIN PRECURSOR V-III REGION
DE (HUMAN);
KW EST
OS Homo sapiens (human)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP 1-400
PA Hillier L., Allen M., Bowles J., Dubouque Y., Geisel G., Gus* S.,
Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
Moore A., Schellenberg K., Stepien M., Tan F., Theising B.,
White Y., Wylie T., Waterston R., Wilson R.,
WashU-Merck EST Project 1997;
RL Unpublished.
CC Contact: WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
CC estw@wustl.edu This clone is available royalty-free through
CC the WashU-Merck EST Project.
CC LSN: contact the IMAGE Consortium (info@imga.lim.gov) for


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FEATURES
Source
Location/Qualifiers
1..324
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site1: Not I; Site2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
/clone="810346"
/clone_lib="Soares ovary tumor NbHOT"
/sex="female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
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/db_xref="GDB:6040648"
BASE COUNT 68 a 102 c 82 g 72 t
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Query Match 49.1%; Score 156; DB 16; Length 324;
Best Local Similarity 92.9%; Pred. No. 4.34e-251;
Matches 196; Conservative 0; Mismatches 10; Indels 5; Gaps 3;
Db 80 acgcagctccagcaccctgtctgtatcccggggaagagcaccctctctcgcagg 139
QY 7 ACCGAGCTCCAGGACCCCTGCTTGTCTCCAGGGGAAGAGCCACCTCTCTCGCAGG 66
Db 140 gccagtcagagtgtagcagcaaa---cttagcctgtaccagcagattcctggccagct 196
QY 67 GCCAGTCACAGTGTAGCAGCAAACTTACCTTACCTGAGTACAGAGACCTGCGCAGGCT 126
Db 197 cccagctctcatctatgtgtatccaccagggccactggtatccaccagcaggttcaga 256
QY 127 CCCAGCTCTCTCATCTATGTGTGATGTCAGAGGGGCACTGCTGATCCACAGAGGTTTCAG- 185
Db 257 tggcagtggtctaggacagagttcactct 287
QY 186 TGGCAGTGGGCTCT-GGGACAGACTTCACCTCT 215

RESULT 10
LOCUS HS1258064 standard; RNA; EST; 324 BP.
AC AA464224;
N1 92189108
DT 13-JUN-1997 (Rel. 52, Created)
DE 2x83c06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810346
DE 5' similar to gb M1740_c4s1 IG KAPPA CHAIN PRECURSOR V-III REGION
DE (HUMAN);
KW EST.
OS Homo sapiens (human)
OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP 1-324
RA Hillier L., Allen M., Bowles L., Dubuque T., Geisels C., Jost S.,
RA Kucaba T., Lucy M., Le N., Lennon G., Marra M., Martin J.,
RA Moore B., Schellenberg K., Steptoe M., Tan F., Theising R.,
RA White Y., Wylie T., Waterston R., Willson R.;
RA WashU-Merck EST Project 1997;
RL Unpublished.
CC Contact: Willson RK WashU-Merck EST Project Washington University
CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
CC MO 63108 Tel: 314 286 1820 Fax: 314 286 1810 Email:
CC estw@wason.wustl.edu This clone is available royalty-free through
CC LNL; contact the IMAGE Consortium (info@image.llnl.gov) for
CC further information. Seq primer: -28m13 rev2 ET from Amersham High
CC quality sequence stop: 161.
FH Key
Location/Qualifiers

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FT source
FT 1..324
FT /organism="Homo sapiens"
FT /note="Organ: ovary; Vector: pT73D (Pharmacia) with a
FT modified polylinker; Site1: Not I; Site2: Eco RI; 1st
FT strand cDNA was primed with a Not I - oligo(dT) primer [5'
FT TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],
FT double-stranded cDNA was size selected, ligated to Eco RI
FT adapters (Pharmacia), digested with Not I and cloned into
FT the Not I and Eco RI sites of a modified pT73 vector
FT (Pharmacia). Library constructed by Bento Soares and
FT M.Fatima Bonaldo."
FT /clone="810346"
FT /clone_lib="Soares ovary tumor NbHOT"
FT /sex="female"
FT /tissue_type="ovarian tumor"
FT /lab_host="DH10B (ampicillin resistant)"
FT <1..>324
FT mRNA
FT Sequence 324 BP; 68 A; 102 C; 82 G; 72 T; 0 other;
Query Match 49.1%; Score 156; DB 63; Length 324;
Best Local Similarity 92.9%; Pred. No. 4.34e-251;
Matches 196; Conservative 0; Mismatches 10; Indels 5; Gaps 3;
Db 80 acgcagctccagcaccctgtctgtatcccggggaagagcaccctctctcgcagg 139
QY 7 ACCGAGCTCCAGGACCCCTGCTTGTCTCCAGGGGAAGAGCCACCTCTCTCGCAGG 66
Db 140 gccagtcagagtgtagcagcaaa---cttagcctgtaccagcagattcctggccagct 196
QY 67 GCCAGTCACAGTGTAGCAGCAAACTTACCTTACCTGAGTACAGAGACCTGCGCAGGCT 126
Db 197 cccagctctcatctatgtgtatccaccagggccactggtatccaccagcaggttcaga 256
QY 127 CCCAGCTCTCTCATCTATGTGTGATGTCAGAGGGGCACTGCTGATCCACAGAGGTTTCAG- 185
Db 257 tggcagtggtctaggacagagttcactct 287
QY 186 TGGCAGTGGGCTCT-GGGACAGACTTCACCTCT 215

RESULT 11
LOCUS AA494059 217 bp mRNA EST 10-JUL-1997
DEFINITION ng61b01.s1 NCI-CGAP_Lip2 Homo sapiens cDNA clone 949241 similar to
gb:X06764 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);
ACCESSION AA494059
NID 92223900
KEYWORDS EST;
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 217)
AUTHORS NCI-CGAP.
TITILE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael P.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 922 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers

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FEATURES

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FT mRNA <1..>217
SQ Sequence 217 BP: 44 A: 75 C: 55 G: 43 T: 0 other:

Query Match      47.5%   Score 151:   DB 67: Length 217:
Best local Similarity 94.9%   Pval No 4 pfc-241:
Matches 161: Conservative    0: Mismatches 16: Indels 0: Gaps

Db          47 acgagactccacaggaccctcgttttcttcacagagaacacagcccctctctctcacaa 106
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Q1          7 ACAGGATCTCCAGACACCGTGTTCCTTCACAGGAAGAACAACAACCTCCTGGTAGS 86
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db          107 gccagtccagagtgtagcaccaagtaattagctctgataccggcgacaagatgcaccaagct 166
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Q1          67 GCCACTCAGAGCTTTAGCAGCAATACATTAGCTTGTAAGCAGCAGACACCTGCACCACT 126
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db          167 gccaggctccctctcttgttgatccacacagggccatctcatccacaa 217
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Q1          127 GCCAAGGTCCTCATCATGATGTCATCATCATGAGGTCATGCAATGCCAGAA 177
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RESULT      13
ID# HS1145281 standard: PNA EST: 260 BP.
NI AA225858;
NI NI 91847166
DT 23-FEB-1997 (Rel. 51, Created)
DT 26-JUL-1997 (Re: 52, last updated, Version 5)
DE nc27d05.sl NCI_CGAP_Prl Homo sapiens cDNA clone 1009353 similar to
DE qb-711894 IG KAPPA CHAIN PRECURSOR V-LII REGION (HUMAN);..
KW EST.
OS Homo sapiens (human)
OC Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
OC Homo.
RN [1]
RP 1-260
RA NCI-CGAP;
RR "National Cancer Institute, Cancer Genome Anatomy Project (CGAP).";
RT Tumor Gene Index";
RL Unpublished.
RC Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: W Marston Linehan,
CC M.D., Rodrigo Chiappe, M.D., Michael Emmert-Buck, M.D., Ph.D. CDNA
CC Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed
CC by Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by:
CC Washington University Genome Sequencing Center Clone Distribution:
CC NCI-CGAP clone distribution information can be found through the
CC I M A G E Consortium/LLNL at:
CC www.bio.llnl.gov/bbrp/image/image.html Insert Length: 1066 Std
CC Error: 0.00 Seq primer: -4m13 fwd. Et from Amersham High quality
CC sequence stock: 250.
FH Key Location/Qualifiers
FI source 1..260
FI /organism="Homo sapiens"
FI /note="Vector: pAMP10 Site_1 Not1 Site_2: EcoRI; 1
FI strand cDNA was primed with oligo(dT)17 on 5' end of
FI RNase-treated, total cellular RNA obtained from
FI 5,000-10,000 microdissected, histologically normal pro
FI epithelial cells Double-stranded cDNA was ligated to
FI adaptors, 5 cycles of PCR applied to the cDNA with an
FI adaptor-specific primer, and the resulting PCR product
FI subcloned into pAMP10 by the ligation method (Life
FI Technologies) Average insert size is 600 bp.NOTE: NO
FI directionally cloned. This library was constructed by
FI Krizman."
FI /clone_id="1009353"
FI /sex="Male"
FI /dev_stage="45 years old"
FI /lab_host="DH10B"
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FT  mRNA
SQ  Sequence 250 bp; 57 A; 84 C; 66 G; 49 T; 4 others;

Query Match      43.1%; Score 137; DB 49; Length 260;
Best Local Similarity 92.2%; Pred. No. 333e-213;
Matches 154; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Db 90 cgcagctccaggccacctgtttgtctccagggaaggagccacctctctctgcaggg 149
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QY 8 CGCAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGAAGAGCCACCCCTCTCTCTGCAGG 67

Db 150 ccaatcagaagtacagcacagatcttagccttagtaccacaaacacctggccaggct 209
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 68 CCAGTCCAGAGTGTACACACAAATTAATTAGCC-TGGTACCAGTAGAGACTTGTCTAGGTT 126

Db 210 ccaggctctcatctatgtctgctccaggaggccactggattccc 256
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 127 CCCAGGCTCCTCATCTATGTGTGTCATCCAGCAGGCGCCACTGGCATCCC 173

RESULT 14
LOCUS      AA225858      260 bp      mRNA      EST      20-JUN-1997
DEFINITION nc27d05.s1 NCI_CGAP_Prl Homo sapiens cDNA clone 3490 similar to
            qb:211894 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION  AA225858
NID        91847166
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
            Homo.
REFERENCE  1 (bases 1 to 260)
AUTHORS   NCI-CGAP.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
            M.D., Michael Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: David B. Krizman, Ph.D.
            cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image.html

Insert Length: 1066 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 250.
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/note="Vector: pAMP10; site.1: NotI; site.2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 500
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
/clone="3490"
/clone_lib="NCI_CGAP_Prl"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
<1..260

Db 93 acgcagctccaggccacctgtttgtctccagggaaggagccacctctctgcaggg 152

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BASE COUNT      57 a      84 c      66 g      49 t      4 others
ORIGIN

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Query Match      43.1%; Score 137; DB 27; Length 260;
Best Local Similarity 92.2%; Pred. No. 333e-213;
Matches 154; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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Db 90 cgcagctccaggccacctgtttgtctccagggaaggagccacctctctgcaggg 149
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QY 8 CGCAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGAAGAGCCACCCCTCTCTCTGCAGG 67

Db 150 ccaatcagaagtacagcacagatcttagccttagtaccacaaacacctggccaggct 209
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 68 CCAGTCCAGAGTGTACACACAAATTAATTAGCC-TGGTACCAGTAGAGACTTGTCTAGGTT 126

Db 210 ccaggctctcatctatgtctgctccaggaggccactggattccc 256
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 127 CCCAGGCTCCTCATCTATGTGTGTCATCCAGCAGGCGCCACTGGCATCCC 173

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```

RESULT 15
LOCUS      AA492131      262 bp      mRNA      EST      10-JUL-1997
DEFINITION ng06092.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone 939218 similar to
            qb:211894 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN).
ACCESSION  AA492131
NID        92221693
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
            Homo.
REFERENCE  1 (bases 1 to 262)
AUTHORS   NCI-CGAP.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: David B. Krizman, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image.html

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Insert Length: 1015 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.

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FEATURES
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1..262
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/organism="Homo sapiens"
/note="Vector: pAMP10; mRNA made from liposarcoma, cDNA
made by oligo-dT priming. Non- directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
/clone="939218"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
<1..262

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BASE COUNT      58 a      90 c      61 g      53 t
ORIGIN

```

```

Query Match      42.1%; Score 134; DB 38; Length 262;
Best Local Similarity 90.6%; Pred. No. 2.95e-207;
Matches 155; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

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Db 93 acgcagctccaggccacctgtttgtctccagggaaggagccacctctctgcaggg 152

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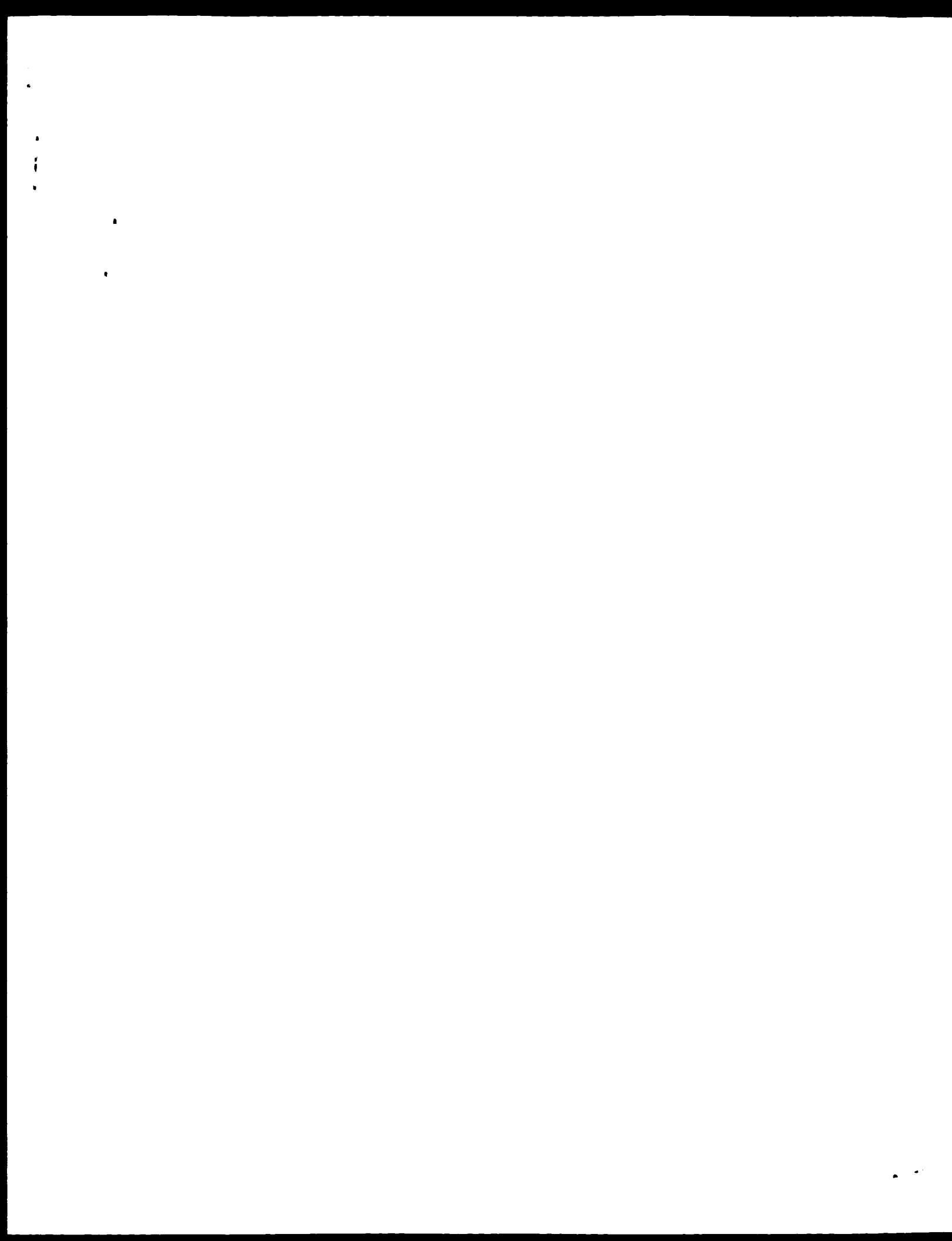
Thu Feb 26 07:04:10 1998

US-08-844-215-15.rstc

Page 9

0Y 7 ACGAGTCTCCAGTAAAGCTTCTTTTCTGTCAGAGGAAGAAGGCAATCTCTCTCTAGAG 66
 Db 153 gccacatcaagactattagcaacagcccaacttaacctggtatatacagcaaaaacgttgcccaagct 212
 0Y 67 GGCATCTGAGAGTGTATAGAGCAATTACTTAACCTGGTGACGACGAGCAACCTGGCCAGGCT 126
 Db 213 cccaaagctccatcaatcatgcatgcatccagcaagctccaatgcatcccaagac 262
 0Y 127 GCGAAGGCTCTCATCTATATGATGAGATGAGAGAGGCTCATTTGCACTCCAGAC 177

Search completed: Tue Feb 24 07:22:48 1998
Job time : 170 secs.



WATERMAN

(M)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSEARCH v3.0 - a database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:15:48 1998: Maxstar time 115.99 seconds
Tabular output not generated 773.214 Million cell updates/sec

Title: SUS-08-844-215-15
Description: (1-318) from US08P44215 seq
Perfect Score: 318
N A Sequence: 1 GAGCTCAGGACGATCTCCAGG
Comp: CFCGAGTGGCTGAGAGAGTCC... CTTGGTTCAGTCTGATTT

Scoring table: TABLE default
Gap 5

Nmatch STD : Phase 0: Query 0

Searched: 397346 seqs, 1410104 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-C
1:EST197 2:EST198 3:EST199 4:EST200 5:EST201 6:EST202
7:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208
13:EST209 14:EST210 15:EST211 16:EST212 17:EST213
18:EST214 19:EST215 20:EST216 21:EST217 22:EST218
23:EST219 24:EST220 25:EST221 26:EST222 27:EST223
28:EST224 29:EST225 30:EST226 31:EST227 32:EST228
33:EST229 34:EST230 35:EST231 36:EST232 37:EST233
38:EST234 39:EST235 40:EST236 41:EST237 42:EST238
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73:EST269 74:EST270 75:EST271 76:EST272 77:EST273
78:EST274 79:EST280 80:EST281 81:EST282 82:EST283
83:EST284 84:EST285 85:EST286 86:EST287 87:EST288
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93:EST294 94:EST295 95:EST296 96:EST297 97:EST298
98:EST299
EST-D
99:EST300 100:EST301 101:EST302 102:EST303 103:EST304
104:EST305 105:EST306 106:EST307 107:EST308 108:EST309
109:EST310 110:EST311 111:EST312 112:EST313 113:EST314
114:EST315 115:EST316 116:EST317 117:EST318 118:EST319
119:EST320

Statistics: Mean 9.864 Variance 1.979 scale 4.985

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description	Pred. No.
1	85.5	273	400	AA156778	EST13471 r1 Soares ova	0.00e+00
2	82.1	261	246	AA200582	EST13472 Testis tumor	0.00e+00
3	79.9	254	400	AA445485	EST13506 Gall Bladder	0.00e+00
4	77.0	245	349	AA479044	EST19199 Skin tumor	0.00e+00
5	72.5	231	435	AA299227	EST19341 Lymph node	0.00e+00
6	66.4	211	328	AA295311	EST100471 Pancreas	0.00e+00
7	66.4	211	328	AA295311	EST100471 Pancreas	0.00e+00
8	58.5	186	370	AA295043	EST100450 Pancreas	0.00e+00
9	57.9	184	377	AA295377	EST100539 Pancreas	0.00e+00
10	57.2	182	363	AA367405	EST178511 Pancreas	0.00e+00
11	57.2	182	363	AA367405	EST178511 Pancreas	0.00e+00
12	55.7	178	289	AA327418	EST103586 Colon	1.55e+294
13	55.7	178	289	AA327418	EST103586 Colon	1.55e+294
14	53.5	170	264	AA366461	EST177478 Pancreas	3.55e+283
15	51.9	165	269	AA344001	EST177478 Pancreas	3.55e+283
16	47.8	152	283	AA361678	EST170983 T-cell lymph	5.44e+273
17	46.9	149	209	AA292250	EST128221 r1 Soares ova	1.52e+244
18	46.9	149	209	AA292250	EST128221 r1 Soares ova	1.52e+244
19	43.1	137	238	AA383014	EST197387 Thymus	1.82e+238
20	43.1	137	238	AA383014	EST197387 Thymus	1.82e+238
21	40.9	130	260	AA225858	EST270518 r1 Not COAP	3.55e+215
22	40.9	130	260	AA225858	EST270518 r1 Not COAP	3.55e+215
23	40.9	130	260	AA225858	EST270518 r1 Not COAP	3.55e+215
24	40.9	130	260	AA225858	EST270518 r1 Not COAP	3.55e+215
25	39.6	126	233	AA300732	EST12847 Testis tumor	3.55e+194
26	39.6	126	233	AA300732	EST12847 Testis tumor	3.55e+194
27	37.7	120	249	AA302152	EST139457 Esophagus	3.33e+182
28	37.7	120	249	AA302152	EST139457 Esophagus	3.33e+182
29	37.4	119	345	AA335086	EST20620 Spleen	3.55e+180
30	37.4	119	345	AA335086	EST20620 Spleen	3.55e+180
31	37.1	118	413	AA301347	EST14279 Testis tumor	3.17e+178
32	36.5	116	352	AA301347	EST14279 Testis tumor	3.17e+178
33	35.2	112	382	AA295796	EST100987 Pancreas	2.52e+161
34	34.0	108	239	AA300732	EST12847 Testis tumor	3.55e+194
35	33.6	107	357	AA361497	EST17040 T-cell lymph	1.87e+156
36	32.7	104	324	AA361497	EST17040 T-cell lymph	1.87e+156
37	32.7	104	324	AA361497	EST17040 T-cell lymph	1.87e+156
38	30.8	98	303	AA300089	EST14031 Testis tumor	5.34e+141
39	30.8	98	303	AA300089	EST14031 Testis tumor	5.34e+141
40	30.8	98	303	AA300089	EST14031 Testis tumor	5.34e+141
41	30.8	98	303	AA300089	EST14031 Testis tumor	5.34e+141
42	30.8	98	303	AA300089	EST14031 Testis tumor	5.34e+141
43	29.9	95	240	AA302152	EST139457 Esophagus	3.33e+182
44	29.9	95	240	AA302152	EST139457 Esophagus	3.33e+182
45	29.9	95	240	AA302152	EST139457 Esophagus	3.33e+182

ALIGNMENTS

RESULT	1	AA156778	400 bp	EST	GENBANK-1997
LOCUS		EST13471 r1 Soares ova		NR017806	EST13471 r1 Soares ova
DEFINITION		5' similar to g13471.15 KAPA CHAIN PROTEIN			5' similar to g13471.15 KAPA CHAIN PROTEIN
ACCESSION		AA156778			
NID		92177199			
KEYWORDS		EST.			
SOURCE		human.			
ORGANISM		Homo sapiens			
REFERENCE		1 (bases 1 to 400)			
AUTHORS		Hillier, L., Allen, M., Bowles, J., Dubouque, J., Geisler, R., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, R., White, Y., Wyllie, T., Waterston, R., and Wilson, R.			
TITLE		WASHU-Merck EST Project 1997			

JOURNAL
COMMENT

Unpublished (1997)

Contact: Wilson RK
Washington University School of Medicine4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28mi3 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES
source1 400
Location/Qualifiers

/organism="Homo sapiens"
/note="Organ: ovary; Vector: p7T3D (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5'
TCTTACCAATCTGAAGTGGAGCGGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."

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/sex="Female"
/tissue_type="ovarian tumor"

/lab_host="DH10B (ampicillin resistant)"
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/db_xref="GDB:5980414"
BASE COUNT 90 a 120 c 106 g 84 t

mRNA

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Best Local Similarity 94.2%; Pred No. 0.00e+00;

Matches 295; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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QY 7 ACCGAGTCTCCAGGACCGCTGTCTTCTCTCCAGGGGGAAGAGCCACCTCTCTCGCAGG 66

Db 130 ccagtcacagttattagcagcagctcttagcttagtaccagcaaacctggcagct 189

QY 67 GCCAGTCACAGCTTTAGCAGCAATTACTTAGCTTGTCTCCAGCAGACCTGGCCAGGCT 126

Db 190 cccaggtctctatcctatgctgcacagcagggcaactggcatcccgagcaggttcagt 249

QY 127 CCGAGTCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 186

Db 250 ggcagtgaggtctgagcagagctctctctcagacacgcggcagagctggagcctgagcttt 309

QY 187 GGCAGTGGGCTTGGGACACACTTCACTTCATCATCAGCA-CAGTGGAGGCTTGAAGATT 245

Db 310 tgcagtgattatctgcacagctatgtagctacgcgtgagcgttgcggcagggagccca 369

QY 246 TGCAGTGATATCTGTCAGCTTTATGCTAACTCAGCTTGGAGCTTGGCCGAGGAGCA 305

Db 370 ggtgggaatacaaa 382

QY 306 GTTGGAGATCAAA 318

RESULT

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

AA300582 346 bp mRNA EST 18-APP-1997

EST13427 Testis tumor Homo sapiens cDNA 5' end similar to

immunoglobulin kappa light chain, VJ regions

AA300582

01952925

EST.

human

ORGANISM

Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia, Eutheria, Primates, Catarrhini, Hominoidea;
Homo.

REFERENCE
AUTHORS

1 (Bases 1 to 346)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Rondon, P.C., Man-Wai, C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitchugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Giles, A., Sneath, C., Hanna, M.C., Hedrick, E., Hinkley, P.S., Jr.,
Kelleys, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanges, P., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, P.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Wiley, J.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hung, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Pannon, M.P., Rosen, C.A., Hasetline, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL

MEDLINE

COMMENT

Other ESTs: THC169106

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavage@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tadb/hgi/hgi.html>)

Seq primer: M3 Reverse

Location/Qualifiers

1..346

/organism="Homo sapiens"

/note="Organ: testis; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI"

/clone_lib="Testis tumor"

/sex="male"

/dev_stage="adult"

<1..>346

BASE COUNT 80 a 92 c 92 g 72 t 10 others

ORIGIN

Query Match 82.1%; Score 261; DB 26; Length 346;

Best Local Similarity 92.8%; Pred. No. 0.00e+00;

Matches 285; Conservative 3; Mismatches 20; Indels 2; Gaps 2;

Db 34 ctcacagggagccctgttttttttcacaggggaaagagccaccttcctgagggcagag 93

QY 14 CTCACAGGACCCCTGTCTTTTCTCTCCAGGGGAAAGAGACCTCTCTCTCTCTCTCTCT 73

Db 94 agagtggttagcagcagctacttagcctgggtaccagaggaacacccctggcagagtcaccagag 153

QY 74 AGAGTGTTAGCAGCAATTAATTAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 133

Db 154 tcttctatggtgctatcccgagggccactggcctccacagagcttcacagagcttcacagag 213

QY 134 TCTCTATCTATCT 193

Db 214 ggtctggggagagcttct 273

QY 194 GGTCTGGGAGAGCTTCT 262

Db 274 tattactgtcagcagctatggtagctcactcactgagcagcttcggccaaagggccagaggttgg 333

QY 253 TATTACTGTACAGCTTTTGTAACTCAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAG 311


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Query Match      77 08. Score 245. DB 52. Length 340.
Best Local Similarity 91.1%; Pred. No. 0.00e+00;
Matches 287; Conservative 0; Mismatches 25; Indels 3; Gaps 3;

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Qy 7 ACCAGTTCACAGCACCCTGTCTTCTCCAGGGGAAAGAGCCACCTCTCTCCAGG 66
Db 88 gccactgaagagtgtagcaaacacttacttagctggtacccacagaaacccctggccaggct 147
Qy 67 GCCAGTCAGAGTGTAGCAGCAATTAATTAGCCTGTGTACCAAGCAGAGACTGGCCAGGT 126
Db 148 ccaaggctctctatgtgtgcatccagcaggggccactggcatccacagacaggttcaagt 207
Qy 127 CCCAGGTCCTCATCATGTGTGTATCCAGCAGGGGCACTGTGTATCCAGCAGGTTCAGT 186
Db 208 ggcagtggtctgggacagacttctcctccaccatcagcagactggagccctgaagatttt 267
Qy 187 GGCAGTGGGTCTGGACAGACTTCATCTCCACCATCAGCAGACTGGAGCCTGAGATTTT 245
Db 268 gcagtatattactgctcaagcagtagtgtagtttaccctcccaantttcgccctggggacc 327
Qy 247 GCAGTATTACTGCTCA-GCTTTTATGTTAACTCAAGT-TGGACGTTGCGCAAGGG-ACC 303
Db 328 acagtgcgatcaaa 342
Qy 304 AAGTGGAGATCAAA 318

RESULT 5
LOCUS AA360223 405 bp mRNA EST 21-APP-1997
DEFINITION EST69341 Lymph node I Homo sapiens cDNA 5' end similar to similar to immunoglobulin kappa light chain, V region.
ACCESSION AA360223
NID 92012543
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata:
Vertebrata: Mammalia: Euthera: Primates: Catarrhini: Hominiidae:
Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,E., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geochagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Keiley,J.M., Kelley,J.C., Liu,I.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.F., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y., Bednarik,D., Peng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Dimke,D., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.P., Rosen,R.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Contact: Kerlavage, AP
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene

```

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Index (http://www.tigr.org/tdb/hgi/hgi.html)
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Location/Qualifiers
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/clone_lib="Lymph node I"
/dev_stage="adult"
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ORIGIN
Query Match 72.6%; Score 231; DB 52; Length 405;
Best Local Similarity 92.1%; Pred. No. 0.00e+00;
Matches 245; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Db 92 ctccaggcaccctgtcttctcaggggaaacagcaccctctctcagggcaccac 151
Qy 14 CTCAGGACCCCTGTCTTCTCCAGGGGAAAGAGCCACCTCTCTCCAGGCTCAATC 73
Db 152 agactgttaggagcttctccttagcctggtaccacagaaacccctggccaggctcc 211
Qy 74 AGAGTGTAGCAGCAATTAATTAGCTGTGTATCCAGCAGGGGCACTGTGTATCCAG 133
Db 212 tctcatctatgtgcatccagcaggggccactggcatccacagacaggttccagtc 271
Qy 134 TCTCATTTATGTGTATCCAGCAGGGGCACTGTGTATCCAGCAGGTTCAGTGTAG 194
Db 272 ggctctggacacacttctcctcancatcagcagactggagccctggaagatttncat 331
Qy 194 GGTCTGGGACAGACTTCATCTCATCATCATCATCATCATCATCATCATCATCAT 254
Db 332 attactgtcactggtatggtagctca 357
Qy 254 ATTACTGTGACGCTTTATGTGTAATCA 274

RESULT 6
LOCUS AA295311 328 bp mRNA EST 18-APP-1997
DEFINITION EST100471 Pancreas tumor I Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, VJ regions.
ACCESSION AA295311
NID 91947646
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes: mitochondrial eukaryotes: Metazoa: Chordata:
Vertebrata: Mammalia: Euthera: Primates: Catarrhini: Hominiidae:
Homo.
REFERENCE 1 (bases 1 to 328)
AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,E., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geochagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Keiley,J.M., Kelley,J.C., Liu,I.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.F., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y., Bednarik,D., Peng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Dimke,D., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.P., Rosen,R.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other_ESTs: THC169106

```

Kozak, D. L., Kunsch, C., Hungtin, J., Li, H., Moiseyev, P. Z., Olson, H., Raymond, L., Welby, F., Wing, J., Xu, C., Yu, C. L., Babcock, M., Dilling, P., Fannon, M. F., Rosen, C. A., Gaslikov, W. A., Fields, C., Fraser, C. M. and Venter, J. C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
95026280
Other EFSs: IHCI68243
Contact: Ketravage, AR
Bioinformatics

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9722 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
fax: 3018699423
Email: arkerlav@tigr.org
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hqi/hqi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers

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/dev_stage="adult"
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			7 others

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Similarity	90.0%		
pred. NC	9.00e-00		

233; Conservative 0; Mismatches 23; Inequal 3; Gaps 11

[illegible]

ccatgcagagctgttagcagcaa - cttagccctggtaccagcagaaacctgcacgca 175

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215

COAGGCTGCTCACTAAGGTGTATTCATAGAGAGGCTATTTGGCACTGATACAGAGGTTTCAGT 186

gcagttgggtctctggacagaggttcactctcaccatcagcagcctacagttctgaattatc: 295

CCAGTGGGTCTGGGACGACGCTTTCATCTCAGGATCAGGAGACCTGGAGGCGGAGATATTT 246

gagtttattactgtcagc 314

CASTGTATTACTGTCAGC 265

AA295277	277 bp	mRNA	EST	19-APR-1997
EST100538		Pancreas tumor I	Homo sapiens	CDNA 5' end similar; 19

immunoglobulin kappa light chain, VJ regions.
AA295377

Q1947711
EST.

human.
Homo sapiens

Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea

Hom3.
1 (bases 1 to 277)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulghner, R.A.,
Ruit, C., Lee, N.H., Kirkness, E.F., Weinstock, G., Gocayne, J.D.,
White, C., Lasker, F., Venter, A., and Weiss, R. (1991) The

CLAYTON, R. A., CLINE, T. R., COTTON, M. D., EARLE-HUGHES, J., FIBER, L. H.,
WILCOX, J., SULLIVAN, R. K., and HARRISON, F. C., Man-wal, Ltd.,
1957, p. 10.

100


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RESULT 10
LOCUS AA29594: 253 bp mRNA EST 18-APR-1997
DEFINITION EST101165 Thymus III Homo sapiens cDNA 5' end similar to
immunoglobulin kappa light chain, V region (GB:Y00640).
ACCESSION AA295941
NID 11948286
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 253)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C.,
Clayton,R.A., Cline,T.P., Cotton,M.D., Earle-Hughes,E., Fink,D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geohagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,P.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudex,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olson,H.,
Raymond,D.L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (5547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
FEATURES
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/note="Organ: thymus. Vector: pBluescript SK-; Site_1"
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/dev_stage="adult"
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Query Match 57.2%; Score 182; DB 25; Length 253;
Best Local Similarity 84.4%; Pred NC 0.000-0.001
Matches 203; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Db 5 actgaacctggtaccagcaagaacctggccaggntccccaggctctctatctatggtgcat 65
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QY 92 ACTTATGCTG55TACACGCAAGACCTG5TATATGCTGCTGACATGATATGATGAT 151
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Db 66 caaccaggccactggtatccagcagcagcttcagtgaggagggtatgggaacagagttca 125
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QY 152 CCAGAG5G5CCACTG5CATCCACAGACAG5TTCAGTGGCAGTG5G5TCTGGGACAGACTTCA 211
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Db 126 ctctcaccatcaggaagcccgcaacttgaagatttaccagttattaccgtcagcagcata 185
|||||
QY 212 CTCACCATCATGACAGACATCGAGCTGAGASATTTTCAGTATGATACGTGTCAGCTTATG 271
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Db 196 aaaaactgcccagagcaactgttctgcccagagagagagagagagagagagagagag 232
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QY 272 GTAAATCATGCTGTTGACGTGTGCGGCAAGGGGACCAAGGTGGAGATCAAA 318
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RESULT 11
LOCUS AA327218 282 bp mRNA EST 20-APR-1997
DEFINITION EST103585 Colon I Homo sapiens cDNA 5' end similar to
immunoglobulin kappa light chain, VNJ regions (GB:Z11844).
ACCESSION AA327218
NID 91979524
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
REFERENCE 1 (bases 1 to 289)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,P.C., Man-Wai,C.,
Clayton,R.A., Cline,T.P., Cotton,M.D., Earle-Hughes,E., Fink,D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geohagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,P.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudex,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
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He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olson,H.,
Raymond,D.L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.P., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (5547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
FEATURES
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Location/Qualifiers
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EcoRI; Site_2: XhoI"
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/dev_stage="adult"
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Best Local Similarity 91.3%; Pred NC 1.55e 29q;
Matches 200; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

Db 72 gttgagcagcagctctcagagcaacactgctgtgtatccagagagagagagagagag 130
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QY 3 GTGTCACAGTGTGACAGTACAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 62
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Db 131 caggagccatcagagctgttatgagcagctatgctatgctatgctatgctatgctatg 190
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QY 63 CAGGGCCAGTGTAGCAGCAATTACTTAGCCTGGTACCAGCAGAGAGCTGGCCA 122
 Db 191 gactccacaggtcgctcatctatgaacacacagagagccactgagcttccacacaggtt 250
 QY 123 GGTCCAGGCTCCCTCATCTATGTGTGATCCAGGAGGCTGCTGCTACCCAGACAGGTT 182
 Db 251 cagtgcactggtgtgagacagacattccactctcaccat 289
 QY 183 CAGTGGCACTGGGTCTGGGACAGACTTCCACTCTCCACCAT 221

RESULT 12
 LOCUS AA295154 264 bp mRNA EST 18-APR-1997
 DEFINITION EST100323 Pancreas tumor I Homo sapiens cDNA 5' end similar to
 immunoglobulin kappa light chain, VJ regions.
 ACCESSION AA295154
 NID Q1947509
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominidae;
 Homo.

REFERENCE 1 (bases 1 to 264)
 AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,P.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
 Clayton,P.A., Cline,T.P., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
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 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Pyder,S.E., Scott,J.L., Sauder,D.M., Shirley,P.,
 Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Raymond,L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
 Dillion,P.J., Fannon,M.B., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M., and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)
 96026280
 Other_ESTS: THC169106
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
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 /dev_stage="adult"
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 BASE COUNT 53 a 74 c 69 g 56 t 7 others
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 Matches 183; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 71 acgcagctccaggaacactgtttgtgtctccaggggaagagccaccctctcaggt 130

QY 7 ACCGAGTCTCCAGGCACTCTCTTTGTCTCTAGGGGAAAGAGACACGCTCTCTCTGAG 66
 Db 131 gccagtnagagtgtagcagcagcactacttagctgtagcagcagaaacacttagcagcaggt 190
 QY 67 GCCAGTCCAGAGTGTATGACGCAATTAATAGCTGGGTAGTACGACAGAGACTGGCTAGGCT 125
 Db 191 cccagggctcctnactatgtgtgcatccagagagggcactggcattccacacagaggttcaat 250
 QY 127 CCCAGGCTCTCATCTATGTGTCATCCAGCAGGAGCTCTGGCATCCACACAGGTTCACT 186
 Db 251 ggcagtgaggctctgg 264
 QY 187 GGCACGTGGCTGTG 200

RESULT 13
 LOCUS AA366461 294 bp mRNA EST 21-APR-1997
 DEFINITION EST177408 Pancreas tumor III Homo sapiens cDNA 5' end similar to
 similar to immunoglobulin kappa light chain, V region.
 ACCESSION AA366461
 NID G2018779
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominidae;
 Homo.

REFERENCE 1 (bases 1 to 294)
 AUTHORS Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fuldner,P.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
 Clayton,P.A., Cline,T.P., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Pyder,S.E., Scott,J.L., Sauder,D.M., Shirley,P.,
 Small,K.V., Spriggs,T.A., Utterback,T.P., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Raymond,L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
 Dillion,P.J., Fannon,M.B., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M., and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
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 96026280
 Other_ESTS: THC168243
 Contact: Kerlavage, AR
 Bioinformatics
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 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse

FEATURES
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 /note="Organ: pancreas; Vector: pBluescript SK-; Site:1;
 EcoRI: Site_2: XhoI"
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Best Local Similarity  98.2%   Prod No. 5,546-2733
Matches 168; Conservative 0; Mismatches 3; Indels 0; Gaps 03

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      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      7  AGCGAGTCTCCAGTACAGTACCTCTCTTCTCTCCAGAGGAGAGAGAGAGAGTCTCTCTCTCTCT 66

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QY      67  GCCAGTCCAGAGTGTTAGCAGCAATTACTTACCTGTGGTACCCAGCAGAGAGACCTTGGCCACAGCT 124

Db      219  ccacaggtcctctcatatgtgtgtcatccagcagagggccactggcattccacagac 269
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DEFINITION	similar to lymphoma homo sapiens CDNA 3 end similar to similar to immunoglobulin kappa, variable region (GF-Y03649).
ACCESSION	A361678
NID	G2013998
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotes: mitochondrial eukaryotes. Metazoa; Chordata. Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 283) Adams M.D., Kertavajae A.R., Fleischmann P.D., Feldner P.A., Eut,C.J., Lee, H., Kirkness, E.F., Weisbach K.S., Gayner, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fible, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Frichman, J.L., Geohagen N.S., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, T.C., Li, L., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, F.F., McDonald, I.A., Nguyen, D.T., Pelligriano, S.M., Phillips, C.A., Pyder, S.E., Scott, I., Saudek, D.M., Shirley, R., Small, K.V., Springs, T.A., Utterback, T.P., Weidman, J., Wiley,

TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL	Nature 377 (5547 Suppl.) 3-174 (1995)
MEDLINE	95026380
COMMENT	Other ESTs: THC168243 Contact: Kerlavage, AR

The Institute for Genomic Research
 9742 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018690506
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES	Source
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BASE COUNT	4 others

Search completed: Tue Feb 24 07:19:36 1998
Job time : 168 secs.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo
 1 (bases 1 to 383)
 REFERENCE
 AUTHORS
 Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A.,
 Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
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 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.P., S.,
 Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
 Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T.,
 Pellegrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L.,
 Saudek, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.R.,
 Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A.,
 Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,
 Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
 Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., J.H., Li, H.,
 Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
 Yu, G.-L., Puben, S.M., Dillon, P.J., Fannon, M.P., Posen, C.A.,
 Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
 TITLE
 Initial Assessment of Human Gene Diversity and Expression Patterns
 JOURNAL
 COMMENT
 Based Upon 52 Million Basepairs of cDNA Sequence
 Unpublished (1995)
 Contact: Venter, J.C.
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@tdb.tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please contact the TIGR Database
 (tdbinfo@tdb.tigr.org).

FEATURES
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LOCUS T29114 381 bp mRNA EST 06-SEP-1995
 DEFINITION EST69430 Homo sapiens cDNA 5' end similar to immunoglobulin light
 chain V(I)J(V) regions (GB 227170) (HT-3121).
 ACCESSION T29114
 NID 9511212
 KEYWORDS EST.
 SOURCE human primer-M13 Reverse library-Human lymphoid tissue.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo
 1 (bases 1 to 381)
 REFERENCE
 AUTHORS
 Adams, M.D., Kerlavage, A.P., Fleischmann, P.D., Fuldner, P.A.,
 Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
 Clayton, P.A., Cline, P.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geohagen, N.S.M.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.P., S.,
 Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
 Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T.,
 Pellegrino, S.M., Phillips, C.A., Pyder, S.E., Scott, J.L.,
 Saudek, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.R.,
 Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A.,
 Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A.,
 Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
 Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., J.H., Li, H.,
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 Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
 TITLE
 Initial Assessment of Human Gene Diversity and Expression Patterns
 JOURNAL
 COMMENT
 Based Upon 52 Million Basepairs of cDNA Sequence
 Unpublished (1995)
 Contact: Venter, J.C.
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@tdb.tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please contact the TIGR Database
 (tdbinfo@tdb.tigr.org).

FEATURES
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 /organism="Homo sapiens"
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 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381

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3
RESULT 127870 383 bp mRNA EST 06-SEP-1995
LOCUS EST19007 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
DEFINITION light chain V region (CB-X06763) (H1-3097)
T27870
ACCESSION 9609958
NID
KEYWORDS
SOURCE human primer-M13 Reverse library-Human lung
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo
1. (bases 1 to 383)
REFERENCE
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, P.D., Fuldner, P.A.,
Bull, C.J., Lee, N., Kirkness, F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J., Georghiades, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.R.P.S.,
Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, J.-I., Marmorek, S.M.,
Merrick, J.M., Moreno-Parlanques, P.F., McDonald, J.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, J.R.,
Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A.,
Coleman, J.A., Collins, F.-J., Dimke, D., Feng, P., Fertig, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Li, H.,
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Yu, G.-L., Yuen, S.M., Dillon, P.J., Fannon, M.P., Posen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
JOURNAL Unpublished (1995)
COMMENT Other ESTs: H1C24452
Contact: Venter, J.C
The Institute for Genomic Research
932 Claffer Rd. Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).
FEATURES
Source Location/Qualifiers
mRNA 1..383
/organism="Homo sapiens"
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Query Match 69.9%; Score 222; DB 58; Length 383;
Best Local Similarity 93.0%; Pred. No. 0 00e+00;
Matches 247; Conservative 0; Mismatches 14; Indels 2; Gaps 2;
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Db 139 gaattattctctctctctctctctctctctctctctctctctctctctctct 197
Gy 74 agactgtttacacacatttctctctctctctctctctctctctctctctctct 133
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QY	74	ACAGGTCCTTAGCAGCAATTTATTAGCTTGGTATGCACAGACAAGATTGGCTAGGCTCCCAAGC	133								
Db	207	tcccatctatcatacatcaccaagggtcacttgacatccccacacagatttcadngcagttt	266								
QY	134	TCCCTATCTATGTGGTCATCCAGCAGGCGCACCTGGCATCCCCAAGAAGGATTCAGTGGCAGTG	193								
Db	267	ggctotggagacagacttttagctctccacatncagtagactggagccctgaagatttttncag	326								
QY	144	GSTTTGGGACAGATT-T-A-TCTTCACAT-CAGCAGAT-TCAGAGTC-TSAAATTTTTTGA	250								
Db	327	tatatattgtccagcagtatgtctaatac	355								
QY	251	TGTATTACTGTC-AGCTTTATGTTAACTC	278								
RESULT	10	T90236	451 bp	mPNA	EST	30-MAR-1995					
LOCUS	DEFINITION	yej5d10.rl Homo sapiens cDNA clone ll1781 5' similar to gb:M12740.fds1 IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN); contains Alu repetitive element;;									
	ACCESSION	T90236									
	NID	g118749									
	KEYWORDS	EST.									
	SOURCE	human clones-ll1781 library-Stratagene lung (#937210) vector-pluescript SK+ host-SOLR cells (kanamycin resistant) primer=M13RP1 Psitcl-EnoPI Psitcl2-XhoI Normal lung tissue from year old male Cloned unidirectionally Primer: Oligo dT Aversin insert size: 1.0 Kb; Uni-ZAP XR Vector, 5' adaptor sequence: 5'-GAATTCGGCAGCAG-3'; 3' adaptor sequence: 5'-CTCGAGTTTCTTTTCTTTT-3'.									
	ORGANISM	Homo sapiens									
	REFERENCE	Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Felidae; Homnidae; Homo.									
	AUTHORS	Hillman,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,I., Tan,F., Trevisan,E., Waterston,P., Williamson,A., Wohlmann,P. and Wilson.P.									
	TITLE	WashU-Merck EST Project									
	JOURNAL	Unpublished (1995)									
	COMMENT	Contact: wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St Louis, MO 63104 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 296 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LNL : contact the IMAGE Consortium (info:image.llnl.gov) for further information Location/Qualifiers 1..451 /organism="Homo sapiens" /clone="ll1781"									
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	Matches	22;	Conservative	0;	Mismatches	15;	Indels	5;	Gaps		
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QY	7	ACGAGATCTCAGACAGCTTTCTTTTGTCTCAGGGAAAAGAGCTATCTCTGCAAG	66								
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QY 127 CCCAGGCTCTCTATGTTGATCCAGCAGGAGGACACTGGCATCCCAAGACAGGTT-CAG 185
Db 250 tgcagtggtgntctgagacagcttactcttcacacatcagcagcctagagcctgaaaga 309
QY 186 TGGAGAGTGGG-TCTGGGACAGAGATTTACTCT-CACCATAGAGAGACTGGAGCTTGAAG-CA 242
Db 310 ttttgcaatttatta 324
QY 243 ITTTGAGTGTATTA 257

RESULT 13
LOCUS R44693 438 bp mRNA EST 26-MAY-1995
DEFINITION Y122599 r1 Homo sapiens cDNA clone 140009 5' similar to gb-M63438
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN):.
ACCESSION P44693
NID g836572
KEYWORDS EST.
SOURCE human clone-140009 library-Soares placenta Nb2HP vector-pT773D
(Pharmacia) with a modified polylinker host-bH10P (ampicillin
resistant) primer-M13P1 Rsite1-Not I Rsite2-Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5].
AACTGGAAGATTCGGCCGACAGATTTTCTTTTCTTTT 3', double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT773
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 438)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Pohlifing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 290
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information
FEATURES
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Location/Qualifiers
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/clone="140009"
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Best Local Similarity 92.6%; Pred No 1 56e-211;
Matches 163; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
Db 1 atggtgatccagagggccactgg-atccagacaggttccagtcagtgaggtctggga 59
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Db 60 cagacttcacttcacacatcagacagactgagcgtctgaagattttgcagtgattactgac 119
QY 203 CAGACTTCATCTCACCATATAGAGACTGGAGCTGAGAGCTTGAAGATTTCATCTCTC 262
Db 120 agcaatatactactaccgtacacatttttggccagggggaccagctggagatcaaa 175

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QY 263 AGCTTTATGGTAACACAGTGGAGCTTGGCCCAAGGAGACAGAGTGGATCAAA 318

RESULT 14
LOCUS R48043 421 bp mRNA EST 18-MAY-1995
DEFINITION YJ66e01.r1 Homo sapiens cDNA clone 153720 5' similar to gb-X06764
IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN):.
ACCESSION R48043
NID g810069
KEYWORDS EST.
SOURCE human clone-153720 library-Soares breast 2NHRst vector-pT773D
(Pharmacia) with a modified polylinker host-bH10P (ampicillin
resistant) primer-M13P1 Rsite1-Not I Rsite2-Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5].
TGTACCAATTCAGATGGGAGGCGCGCTTTTCTTTTCTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT773 vector (Pharmacia). Library went through one round
of normalization to a cdt = 230. Library constructed by Bento
Soares and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 421)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Pohlifing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 242
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information
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/clone="153720"
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Best Local Similarity 91.7%; Pred No 2 04e-135;
Matches 176; Conservative 0; Mismatches 12; Indels 4; Gaps 4;
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QY 74 AGAGTGTAGCAGCAATTAATTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 133
Db 195 tctcatctatgtatcatccaccagggcagcagcagcagcagcagcagcagcagcagcagc 254
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QY 190 AGTGGGTCTGGG 201

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Search completed: Tue Feb 24 07:15:25 1998
Job time : 292 secs.

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RESULT 15
LOCUS Y71607.1 Homo sapiens cDNA clone 154165, 5' similar to
DEFINITION gb:M12740_cds1 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN)..
ACCESSION R51922
NID 981824
KEYWORDS EST:
SOURCE human clone-154165 library-Soares breast 2NbHst vector-pT73D
(Pharmacia) with a modified polylinker host-DH10B (ampicillin
resistant) primer-M13Rpl Rsite1-Not I Rsite2-Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dI) primer [5'
TGTAAGCAATCTGAGAGGAGGCGCCGCTTTTCTTTTCTTTT 3'].
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 230. Library constructed by Bento
Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 361)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Holtman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Pfinkel, L., Rohlfing, J., Soares, M., Tan, P.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 308
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information
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/clone="154165"

BASE COUNT 75 a 108 c 91 g 83 t 4 others
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Matches 221; Conservative 0; Mismatches 24; Indels 11; Gaps 10;

Db 91 ctccagccaccctgtctgtctgtctcgggggaaagaatcaccctctctctcaggggccactc 150
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Db 151 aaagtgtt-gc--caacaacttagctctatccagcagaaacacctgggcccaggctcccagg 207
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Db 208 ctctcatctatctgtctgtctcaccaggggccctgtgtatccagccaggttccagtggg 267
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QY 133 CTTCCATCACTATGGTG-TATCATAATAGAT-TCAATGGAT-CCAGAGATAGATAGATGG- 188
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Db 268 cagtgggtctctggagagagatttcatttcacatccagcagcctcagctcttgaagattt 327
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 189 CATGGAG-TTGGAG-ACAGAT-TTCACTTCACTATCAATCAATCAATCAATCAATCAAT 245
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

Db 328 tgcattctattattgt 343
||||| ||||||| ||
QY 246 TGCAGTGTATTACTGT 261

```



W P E R L F

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit,
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MPSrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 13:44:51 1998, Master time 19.76 Seconds
Tabular output not generated.
740,131 Million cell updates/sec

Title: >US-08-844-215-15
Description: (1-318) from US08844215.seq
Perfect Score: 318
N.A. Sequence: 1 GAGCTCACCGACGTCGACG
Comp: CTCGAGTGGTCGAGAGTCC GAGCCAGGTGGACATCAAA 318
CGCTGTCACCTCTAGTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0: Query 0
Searched: 87531 seqs, 2294601 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:569 9:5691
10:5612 11:5613 12:5614 13:5615 14:5616

Statistics: Mean 7.613 Variance 4.275: scale 1.781

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
Result No.	Score	Query Match	Description	Pred. No.	
1	272	95.5	Sequence 1, Application 1	1	940-181
2	253	82.7	Sequence 2, Application 2	1	160-174
3	263	82.7	Sequence 3, Application 3	1	160-174
4	263	82.7	Sequence 4, Application 4	1	160-174
5	262	82.4	Sequence 5, Application 5	1	160-174
6	218	58.5	Sequence 6, Application 6	1	160-174
7	215	57.9	Sequence 7, Application 7	1	160-174
8	215	57.5	Sequence 8, Application 8	1	160-174
9	215	57.5	Sequence 9, Application 9	1	160-174
10	215	57.5	Sequence 10, Application 10	1	160-174
11	215	57.5	Sequence 11, Application 11	1	160-174
12	215	57.5	Sequence 12, Application 12	1	160-174
13	215	57.5	Sequence 13, Application 13	1	160-174
14	215	57.5	Sequence 14, Application 14	1	160-174
15	215	57.5	Sequence 15, Application 15	1	160-174
16	142	44.7	Sequence 16, Application 16	1	160-174
17	141	44.3	Sequence 17, Application 17	1	160-174
18	135	42.5	Sequence 18, Application 18	1	160-174
19	135	42.5	Sequence 19, Application 19	1	160-174

20 130 40.9 321 7 US-08-425 Sequence 72, Application 1,290-76
21 130 40.9 321 10 PCT-US92-0 Sequence 74, Application 1,290-76
22 130 40.9 321 5 US-07-988 Sequence 74, Application 1,290-76
23 130 40.9 321 7 US-08-425 Sequence 74, Application 1,290-76
24 130 40.9 321 7 US-08-425 Sequence 74, Application 1,290-76
25 130 40.9 321 10 PCT-US92-0 Sequence 74, Application 1,290-76
26 130 40.9 321 5 US-07-988 Sequence 74, Application 1,290-76
27 130 40.9 321 5 US-07-988 Sequence 74, Application 1,290-76
28 130 40.9 321 10 PCT-US92-0 Sequence 74, Application 1,290-76
29 127 39.9 333 11 PCT-US93-0 Sequence 9, Application 2,020-73
30 127 39.9 333 11 PCT-US93-0 Sequence 9, Application 2,020-73
31 126 39.6 384 6 US-08-468 Sequence 13, Application 1,080-72
32 126 39.6 384 6 US-08-468 Sequence 13, Application 1,080-72
33 125 39.3 330 7 US-08-470 Sequence 20, Application 5,930-72
34 125 39.3 330 13 PCT-US95-1 Sequence 20, Application 5,930-72
35 125 39.3 330 7 US-08-467 Sequence 20, Application 5,930-72
36 125 39.3 5703 7 US-08-467 Sequence 50, Application 5,830-72
37 125 39.3 5703 13 PCT-US95-1 Sequence 50, Application 5,830-72
38 124 39.0 590 7 US-08-300 Sequence 62, Application 3,130-71
39 124 39.0 590 7 US-08-300 Sequence 62, Application 3,130-71
40 124 39.0 590 13 PCT-US95-1 Sequence 62, Application 3,130-71
41 124 39.0 321 10 PCT-US92-0 Sequence 71, Application 3,130-71
42 124 39.0 321 5 US-07-988 Sequence 71, Application 3,130-71
43 124 39.0 321 7 US-08-425 Sequence 69, Application 3,130-71
44 124 39.0 549 1 545090-4 Patent No. 545090
45 123 38.7 5238 1 5453363-1 Patent No. 5453363 1,680-70

ALIGNMENTS

RESULT 1
ID PCT-US93-12501-1 STANDARD: DNA: UNC: 325 RP
AC XXXXX
DT 01-JAN-1900
CC Sequence 1, Application PCT-US93-12501
CC Sequence 1, Application PCT-US93-12501
CC GENERAL INFORMATION:
CC APPLICANT: Chang, Tse Wen
CC TITLE OF INVENTION: ALLERGEN-SPECIFIC IGA MONOCLONAL ANTIBODIES AND
CC TITLE OF INVENTION: RELATED PROPHETIS FOR ALLERGY TREATMENT
CC NUMBER OF SEQUENCES: 10
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Tanox Biosystems, Inc.
CC STREET: 10301 Stella Link Rd.
CC CITY: Houston
CC STATE: Texas
CC COUNTRY: USA
CC ZIP: 77025
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Hi Density Diskette
CC COMPUTER: IBM PS/2
CC OPERATING SYSTEM: DOS, Version 3.30
CC SOFTWARE: Wordperfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER PCT/US93/12501
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mirabel, Eric P.
CC REGISTRATION NUMBER: 31,211
CC REFERENCE/DOCKET NUMBER: TMX92-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 713-664-2288
CC TELEFAX: 713-664-8914
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 325 nucleotides
CC TYPE: nucleic acid
CC STRANDEDNESS: double stranded
CC TOPOLOGY: Linear

CC STREET: One Market Plaza, Steuart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM: disk
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC PREFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 182:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 900 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: Join(116..163, 351..650)
CC Sequence 900 BP: 220 A; 241 C; 201 G; 238 T; 0 other;

Query Match 82.4%; Score 262; DB 7; Length 900;
Best Local Similarity 97.8%; Pred. No. 6,58e-174;
Matches 268; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 375 ACCAGTCTCCAGGACCTGCTTTGTCTCCAGGGGAAGAGCCCTCTCTCGCAGG 434
QY 7 ACCAGTCTCCAGGACCTGCTTTGTCTCCAGGGGAAGAGCCCTCTCTCGCAGG 66
Db 435 GCCAGTCAGAGTGTAGCAGCAGCTACTTAGCTGTGACAGAGAAACCTGCCAGGCT 494
QY 67 GCCAGTCAGAGTGTAGCAGCAGCTACTTAGCTGTGACAGAGAAACCTGCCAGGCT 126
Db 495 CCGAGGCTCTCATCTATGCTGATCCAGAGGGGACCTGGCATCCAGACAGGTTTCAGT 554
QY 127 CCGAGGCTCTCATCTATGCTGATCCAGAGGGGACCTGGCATCCAGACAGGTTTCAGT 186
Db 555 GGCAGTGGGTCTGGGACAGACTTCTATGATCCAGAGGGGACCTGGCATCCAGAGGTTTCAGT 614
QY 187 GGCAGTGGGTCTGGGACAGACTTCTATGATCCAGAGGGGACCTGGCATCCAGAGGTTTCAGT 246
Db 615 GCAGTGTATTACTGTGACGAGTATGTTAGCTCAG 648
QY 247 GCAGTGTATTACTGTGACGAGTATGTTAGCTCAG 280

RESULT 6
ID US-08-053-131-178 STANDARD: DNA: UNC: 812 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 178, Application US/08053131.
CC Sequence 178, Application US/08053131

CC Patent No. 5661016
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC PREFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 178:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 812 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: Join(199..246, 418..714)
CC Sequence 812 BP: 201 A; 225 C; 187 G; 199 T; 0 other;

Query Match 68.6%; Score 218; DB 7; Length 812;
Best Local Similarity 95.0%; Pred. No. 7.11e-141;
Matches 246; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

Db 442 ACACAGTCTCCAGGACCTGCTTTGTCTCCAGGGGAAGAGCCCTCTCTCGCAGG 501
QY 7 ACACAGTCTCCAGGACCTGCTTTGTCTCCAGGGGAAGAGCCCTCTCTCGCAGG 66
Db 502 GTCAGTCTCAGAGTGTAGCAGCAGCTACTTAGCTGTGACAGAGAAACCTGCCAGGCT 558
QY 67 GTCAGTCTCAGAGTGTAGCAGCAGCTACTTAGCTGTGACAGAGAAACCTGCCAGGCT 126
Db 559 CCGAGGCTCTCATCTATGCTGATCCAGAGGGGACCTGGCATCCAGACAGGTTTCAGT 618
QY 127 CCGAGGCTCTCATCTATGCTGATCCAGAGGGGACCTGGCATCCAGACAGGTTTCAGT 186
Db 619 GGCAGTGGGTCTGGGACAGACTTCTATGATCCAGAGGGGACCTGGCATCCAGAGGTTTCAGT 678
QY 187 GGCAGTGGGTCTGGGACAGACTTCTATGATCCAGAGGGGACCTGGCATCCAGAGGTTTCAGT 246
Db 679 GCAGTGTATTACTGTGACG 697
||||| |||||||

RESULT 11
ID US-08-276-852-158 STANDARD: DNA: UNC: 729 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 158, Application US/08276852.
CC Sequence 158, Application US/08276852.
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 565219th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 158:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 729 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
SQ Sequence 729 BP, 156 A, 192 C, 208 G, 173 T, 0 other.

Query Match 67.6%; Score 215; DB 7; Length 729;
Best Local Similarity 84.1%; Pred. No. 1,25e-138;
Matches 265; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 338 TTTCCTCTCAGTTGTCGCTGCGCCAAAGTATACAGAGAGTACATAGACATACACA 397
Cc 318 TTGATCTCCACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 259

Db 398 GTATACATGCAAAATCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 457
Cc 258 GTATACATGCAAAATCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199

Db 458 AGACGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 517
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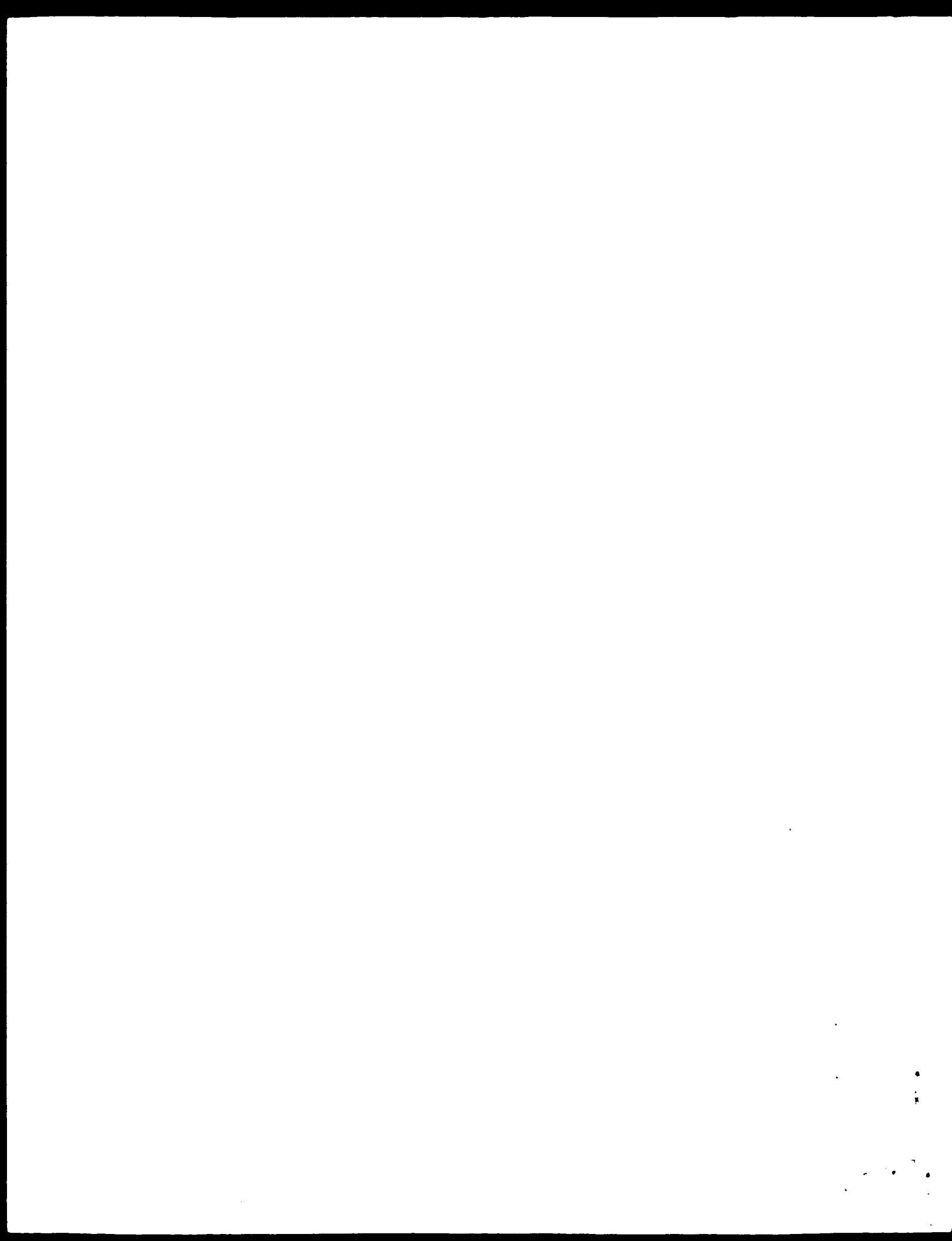
Db 518 GATCAACCTTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 577

Cp 138 GAGGAGCTGGAGGCTTGGGAGGCTTGGGAGGCTTGGGAGGCTTGGGAGGCTTGGGAGG 79
Cc 578 GCTGTGACTGACCTTACAGGAGAGAGGAGAGAGGAGAGAGGAGAGAGGAGAGAGG 647
Cc 78 ACTCTGATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19
Cc 638 TGGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 652
Cc 18 TGGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4

RESULT 12
ID US-08-276-852-155 STANDARD: DNA: UNC: 13254 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 156, Application US/08276852.
CC Sequence 156, Application US/08276852.
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 565219th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCR1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 156:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 13254 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: circular
CC MOLECULE TYPE: DNA (genomic)
SQ Sequence 13254 BP, 3206 A, 3559 C, 3251 G, 3238 T, 0 other.

Query Match 67.6%; Score 215; DB 7; Length 13254;
Best Local Similarity 84.1%; Pred. No. 1,25e-138;
Matches 265; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Db 12606 TTTCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1605
Cc 4 GATCAACCTTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64



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RESULT 13
ID KV3J_HUMAN STANDARD: PRT: 116 AA.
AC P04434;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85087932.
RA PECH M., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR EMBL: X02723; ; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3HUVH.
DR HSSP: P01607; IMCP.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION (VH).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 55 FRAMEWORK 2.
FT DOMAIN 56 70 FRAMEWORK 3.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116
SQ SEQUENCE 116 AA; 12757 MW; 27FA1BCE CRC32;

Query Match 74.3%; Score 548; DB 5; Length 116;
Best Local Similarity 86.4%; Pred. No. 3.01e-98;
Matches 76; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

Db 24 mtasptslspervtlscrasqsvssyltwyqkpkqaprllygastratsiparf 83
Qy 3 LTQSPATLSLSPGERATLSCRASQSVNK-YLAWYQKPKQAPRLLYDASNPAIGIPARF 61
Db 84 sgsqsgtdftltisslqpedfavyycq 111
Qy 62 SGSGSGTDFLTLSNLEPEDFAVYVCQ 89

RESULT 14
ID KV1M_HUMAN STANDARD: PRT: 108 AA.
AC P01605;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-I REGION (LAV).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 77038198.
RA CAPRA J.D., KLAPPER D.G.;
RL SCAND. J. IMMUNOL. 5:677-684(1976).
CC -!- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE
CC IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH
CC WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01871; K1HULY.
DR HSSP: P01607; 2FCW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 55 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.

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FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 22282B0C CRC32;

Query Match 73.6%; Score 543; DB 5; Length 108;
Best Local Similarity 67.6%; Pred. No. 4.32e-97;
Matches 71; Conservative 21; Mismatches 12; Indels 1; Gaps 1;

Db 3 qmtqpslsvsdvdrvtitocsqgnvnaylnwyqkpkglapkllygastratvpsrf 62
Qy 2 ELTQSPATLSLSPGERATLSCRASQSVNKYLAWYQKPKQAPRLLYDASNPAIGIPARF 61
Db 63 sgsqsgtdftltisslqpediatyycqgnnnwptfgqqtkev 107
Qy 62 SGSGSGTDFLTLSNLEPEDFAVYVCQORSQDWV-TFGGGIKVEIK 105

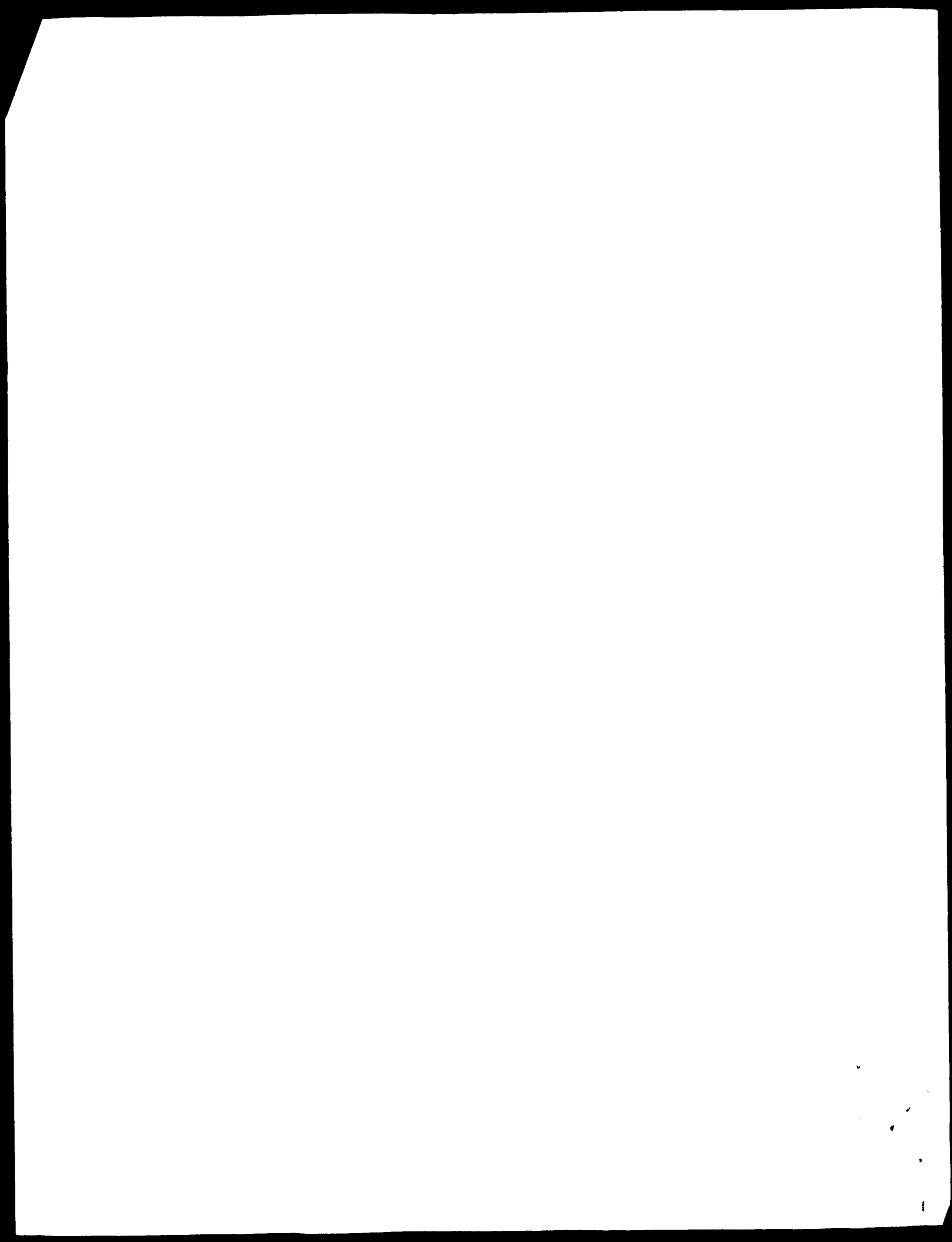
RESULT 15
ID KVID_HUMAN STANDARD: PRT: 107 AA.
AC P01596;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-I REGION (CAR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 75075135.
RA MILSTEIN C.P., DEVORSON E.V.;
RL EUR. J. BIOCHEM. 49:377-391(1974).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (1.2) MARKER.
CC PIR: A01864; K1HUAR.
DR HSSP: P01607; IDFB.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT CARBOHYD 28
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; 04RF9EFD CRC32;

Query Match 71.1%; Score 525; DB 5; Length 107;
Best Local Similarity 63.5%; Pred. No. 6.22e-93;
Matches 66; Conservative 23; Mismatches 15; Indels 0; Gaps 0;

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Db 63 sgsqsgtdftltisslqpbfbatycqyntfffgatkvdk 106
Qy 62 SGSGSGTDFLTLSNLEPEDFAVYVCQORSQDWVTFGGIKVEIK 105

Search completed: Tue Feb 24 07:19:20 1998
Job time : 15 secs.

```



WIREH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:19:37 1998: Maspar time 9.55 Seconds
334.962 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-9
Description: (1-105) from US08A44215 pep
Perfect Score: 738
Sequence: 1 AELTQSPATLSLSPGERATL.....YCCQPSDWVTFGGIKVEIK 105

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30469580 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

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8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann11 16:unann12 17:unann13
18:unrev

Statistics: Mean 40.220; Variance 128.295; scale 0.313
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	695	94.2	Ig kappa chain V reg 1 85e-71
2	689	93.4	Ig kappa chain V reg 1 10e-70
3	698	91.9	Ig kappa chain V reg 2 87e-69
4	675	91.5	Ig kappa chain V reg 6 99e-69
5	671	90.9	Ig kappa chain V reg 2 29e-68
6	657	89.0	Ig kappa light chain 1 44e-66
7	656	88.9	Ig kappa light chain 1 94e-66
8	655	88.8	Ig kappa light chain 2 61e-66
9	649	87.9	Ig kappa chain V reg 1 54e-65
10	641	86.9	Ig kappa chain V reg 1 64e-64
11	631	85.5	Ig kappa chain V reg 3 14e-63
12	626	84.8	Ig kappa chain V reg 1 37e-62
13	626	84.8	Ig kappa chain - hum 1 37e-62
14	620	84.0	Ig kappa chain V reg 8 06e-62
15	617	83.6	Ig kappa chain V reg 1 95e-61
16	615	83.3	Ig kappa chain V reg 3 52e-61
17	614	83.2	Ig kappa chain V reg 4 72e-61
18	612	82.9	Ig kappa chain - hum 8 52e-61
19	611	82.8	Ig kappa chain V reg 1 14e-60
20	611	82.7	Ig kappa chain V reg 1 14e-60

21	610	82.7	104	7	PH0964	Ig kappa chain V reg 1 54e-60
22	610	82.7	107	7	S34005	Ig kappa chain V reg 1 54e-60
23	609	82.5	109	7	B30602	Ig kappa chain V reg 2 06e-60
24	608	82.4	108	7	C30608	Ig kappa chain V reg 2 77e-60
25	608	82.4	109	7	G30607	Ig kappa chain V reg 2 77e-60
26	608	82.4	129	2	K3H0H1	Ig kappa chain V reg 2 77e-60
27	607	82.2	109	7	F44151	Ig kappa chain V reg 3 71e-60
28	606	82.1	109	7	C30601	Ig kappa chain V reg 4 99e-60
29	605	82.0	109	7	F30601	Ig kappa chain V reg 6 49e-60
30	605	82.0	109	2	K3H0S1	Ig kappa chain V reg 6 49e-60
31	604	81.8	109	7	F30607	Ig kappa chain V reg 8 48e-60
32	604	81.9	129	2	K3H0HA	Ig kappa chain V reg 8 98e-60
33	603	81.7	110	7	S20635	Ig kappa chain V reg 1 21e-59
34	602	81.6	109	7	PH0963	Ig kappa chain V reg 1 62e-59
35	601	81.4	130	7	S40360	Ig kappa chain - hum 2 17e-59
36	600	81.3	109	7	F30601	Ig kappa chain V reg 2 42e-59
37	600	81.3	109	2	K3H0WL	Ig kappa chain V reg 2 52e-59
38	599	81.2	109	7	G30601	Ig kappa chain V reg 3 91e-59
39	599	81.2	109	7	H30601	Ig kappa chain V reg 3 91e-59
40	596	80.8	109	2	K3H0T1	Ig kappa chain V reg 5 46e-59
41	595	80.6	109	7	S47181	Ig kappa chain - hum 1 27e-58
42	595	80.6	110	7	F30607	Ig kappa chain V reg 1 27e-58
43	592	80.2	109	2	K3H0PM	Ig kappa chain V reg 3 67e-58
44	591	80.1	129	7	S46369	Ig light chain V reg 4 12e-58
45	591	80.1	134	7	S38643	Ig kappa chain V reg 4 12e-58

ALIGNMENTS

RESULT 1
ENTRY G44151 #type fragment
TITLE Ig kappa chain V region (JM-10) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jun-1994 #sequence_revision 27-Jun-1994 #ext_change 15-Aug-1996

ACCESSIONS G44151
REFERENCE A44151
#authors Zebadee, S L ; Barbas III, C F ; How, Y I ; Caethien, R H ;
Graff, P ; Dedraw, J ; Pyati, J ; Lapolla, P ; Burton,
D P ; Lerner, P A ; Thornton, G B.
#journal Proc. Natl. Acad. Sci. U S A (1992) 89:3175-3179
#title Human combinatorial antibody libraries to hepatitis B surface antigen.
#accession G44151
#status preliminary: not compared with conceptual translation
#molecule_type mRNA
#residues 1-108 #label ZEB
#note nucleotide translation not given
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 108 #checksum 770

Query Match	94.2%	Score 695	DB 7	Length 108
Best Local Similarity	93.4%	Pred. No. 1.85e-71		
Matches	99	Conservative	4	Mismatches
			2	Indels
			1	Gaps
DB	1	aeltqspatlsdpgeratlsctasgssvslawyqkpgqaprllydasnratpaipar 60		
QY	1	AELTQSPATLSLSPGERATLSCTASGSSVSNVYLAWYQKPGQAPRLLYIASNPAIGIPAR 60		
DB	61	fsggsgtdftltisslepedafvyyqgqsnwffsfgggtkveik 106		
QY	61	FSGSGTDFTTISNLEPEDAFVYVYQGSNWFFSGGTFKVEIK 105		
RESULT 2				
ENTRY PL0106 #type fragment				
TITLE Ig kappa chain precursor V-J-C region (IS1) - human (fragment)				
ORGANISM #formal_name Homo sapiens #common_name man				
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #ext_change 16-Aug-1996				
ACCESSIONS PL0105				

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REFERENCE
  #authors      Silverstein, L.E.; Litwin, S.; Carmack, C.E.
  #journal      J. Exp. Med. (1989) 169:1631-1643
  #title        Relationship of variable region genes expressed by a human B
                cell lymphoma secreting pathologic anti-Pr-2 erythrocyte
                autoantibodies.
  #cross-references MUID:89235583
  #accession      PLO106
  #molecule_type mRNA
  #residues       1-144 #label SIL
CLASSIFICATION   #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS          heterotetramer; immunoglobulin
FEATURE
  1-20             #domain signal sequence #status predicted #label SIG\
  21-115           #domain V region #label VRE\
  44-54            #region complementarity-determining 1\
  70-76            #region complementarity-determining 2\
  109-115          #region complementarity-determining 3\
  116-127          #domain J region #label JRG\
  128-144          #domain C region (fragment) #label CPE
  SUMMARY         #length 144 #checksum 3623

Query Match      93.4%; Score 689; DB 7; Length 144;
Best Local Similarity 93.3%; Pred. No. 1.10e-70;
Matches 97; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Db 24 ltqspatlsppgeratlscrasqsvsyawygqpgqaprllydasnratgiparfs 83
   |||||
QY 3 LTQSPATLSLSPGERATLSCPASQSVNKKYAWYQQPGQAPRLIYDASNRPATGIPARFS 62
   |||||

Db 84 gsgsgtdftltisslepedfavyycqgrsnwpltfgggtkveik 127
   |||||
QY 63 GSGSGTDFLTISNLEPEDFAVYCYQQRSDW-VTFGGTKVEIK 105

RESULT 3
ENTRY      S23628 #type fragment
TITLE      Ig kappa chain V region - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
          16-Aug-1996
ACCESSIONS S23628
REFERENCE   S23623
AUTHORS     Olee, T., Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.;
            Kozin, F.; Carson, D.A.; Chen, P P
JOURNAL     J. Exp. Med. (1992) 175:831-842
TITLE       Genetic analysis of self-associating immunoglobulin G
            rheumatoid factors from two rheumatoid synovia implicates
            an antigen-driven response.
  #cross-references MUID:92156804
  #accession      S23628
  #status         preliminary
  #molecule_type DNA
  #residues       1-111 #label OLE
  #cross-references EMBL:X59705
CLASSIFICATION   #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS          heterotetramer; immunoglobulin
SUMMARY         #length 111 #checksum 3907

Query Match      91.9%; Score 678; DB 7; Length 111;
Best Local Similarity 93.3%; Pred. No. 2.87e-69;
Matches 97; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Db 4 ltqspatlsppgeratlscrasqsvsyawygqpgqaprllydasnratgiparfs 63
   |||||
QY 3 LTQSPATLSLSPGERATLSCPASQSVNKKYAWYQQPGQAPRLIYDASNRPATGIPARFS 62
   |||||

Db 64 gsgsgtdftltisslepedfavyycqgrsnwpltfgggtkveik 107
   |||||
QY 63 GSGSGTDFLTISNLEPEDFAVYCYQQRSDW-VTFGGTKVEIK 105

RESULT 4
ENTRY      S40379 #type complete
TITLE      Ig kappa light chain (VJ) - human

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ENTRY      A56701 #type fragment
TITLE      Ig kappa chain V region precursor (HuA) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
          09-May-1997
ACCESSIONS A56701
REFERENCE   A56701
AUTHORS     Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat,
            E.A.
JOURNAL     J. Biol. Chem. (1995) 270:12457-12465
TITLE       Human and mouse monoclonal antibodies to blood group A
            substance, which are nearly identical immunochemically, use
            radically different primary sequences.
  #accession      A56701
  #status         preliminary
  #molecule_type mRNA
  #residues       1-128 #label NIC
  #cross-references GB:L41174
CLASSIFICATION   #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS          heterotetramer; immunoglobulin
SUMMARY         #length 128 #checksum 6378

Query Match      91.5%; Score 675; DB 7; Length 128;
Best Local Similarity 92.3%; Pred. No. 6.99e-69;
Matches 96; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

Db 24 ltqspatlsppgeratlscrasqsvsyawygqpgqaprllydasnratgiparfs 83
   |||||
QY 3 LTQSPATLSLSPGERATLSCPASQSVNKKYAWYQQPGQAPRLIYDASNRPATGIPARFS 62
   |||||

Db 84 gsgsgtdftltisslepedfavyycqgrsnwprsfgggtkveik 127
   |||||
QY 63 GSGSGTDFLTISNLEPEDFAVYCYQQRSDW-VTFGGTKVEIK 105

RESULT 5
ENTRY      S54905 #type fragment
TITLE      Ig kappa chain V region - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
          16-Aug-1996
ACCESSIONS S54905
REFERENCE   S54905
AUTHORS     Esposito, G.; Traboni, C.
SUBMISSION Submitted to the EMBL Data Library, November 1994
DESCRIPTION Cloning and sequencing of cDNA coding for the variable
            domains of a human antibody against Hepatitis C virus
            helicase.
  #accession      S54905
  #status         preliminary
  #molecule_type mRNA
  #residues       1-114 #label ESP
  #cross-references EMBL:X82934
CLASSIFICATION   #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS          heterotetramer; immunoglobulin
SUMMARY         #length 114 #checksum 5831

Query Match      90.9%; Score 671; DB 7; Length 114;
Best Local Similarity 91.4%; Pred. No. 2.29e-68;
Matches 96; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Db 4 mtqspatlsppgeratlscrasqsvsyawygqpgqaprllydasnratgiparfs 63
   |||||
QY 3 LTQSPATLSLSPGERATLSCPASQSVNKKYAWYQQPGQAPRLIYDASNRPATGIPARFS 62
   |||||

Db 64 gsgsgtdftltisslepedfavyycqgrsnwpltfgggtkveik 108
   |||||
QY 63 GSGSGTDFLTISNLEPEDFAVYCYQQRSDW-VTFGGTKVEIK 105

RESULT 6
ENTRY      S40379 #type complete
TITLE      Ig kappa light chain (VJ) - human

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ORGANISM      *formal_name Homo sapiens *common_name man
DATE          19-May-1994 *sequence_revision 26-May-1995 *text_change
16-Aug-1996
ACCESSIONS    S40379
REFERENCE      Klein, R.; Jaenichen, R.; Zachau, H.G.
              Eur. J. Immunol. (1993) 23:3248-3271
              Expressed human immunoglobulin chi genes and their
              hypermutation.
*accession    S40379
**status      preliminary: translation not shown
**molecule_type mRNA
**residues     1-128 *label KLE
**cross-references EMBL:X72459
CLASSIFICATION *superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS       heterotetramer: immunoglobulin
SUMMARY        #length 128 *molecular-weight 14213 #checksum 5928

Query Match      89.0%; Score 657; DB 7; Length 128;
Best Local Similarity 90.4%; Pred. No. 1.44e-66;
Matches 94; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Db 24 ltqspatlsppgeratlsctasqsvsyawyyqkspqprlliyasratgiparfs 83
|||||
Qy 3 LTQSPATLSLSPGERATLSCTASQSVNKYLAWYQCKPQAPPLIYDASNPAITGIPAPFS 62
|||||

Db 84 gsgsgtdftltisslepedfavyycqgrskwptfagggtkvek 127
|||||
Qy 63 GSGSGTDFLTISNLEPEDFAVYCCQPSDW-VTFGGTKVEIK 105
|||||

RESULT 7
ENTRY      S40345 *type complete
TITLE      Ig kappa light chain (VJC) - human
ORGANISM   *formal_name Homo sapiens *common_name man
DATE       19-May-1994 *sequence_revision 26-May-1995 *text_change
16-Aug-1996
ACCESSIONS S40345
REFERENCE   Klein, R.; Jaenichen, R.; Zachau, H.G.
              Eur. J. Immunol. (1993) 23:3248-3271
              Expressed human immunoglobulin chi genes and their
              hypermutation.
*accession S40345
**status    preliminary: translation not shown
**molecule_type mRNA
**residues  1-128 *label KLE
**cross-references EMBL:X72455
CLASSIFICATION *superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS       heterotetramer: immunoglobulin
SUMMARY        #length 128 *molecular-weight 13983 #checksum 6271

Query Match      88.9%; Score 656; DB 7; Length 128;
Best Local Similarity 89.6%; Pred. No. 1.94e-66;
Matches 95; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

Db 20 ltqspatlsppgeratlsctasqsvsyawyyqkspqprlliyasratgiparfs 79
|||||
Qy 3 LTQSPATLSLSPGERATLSCTASQSVNKYLAWYQCKPQAPPLIYDASNPAITGIPAPFS 62
|||||

Db 80 gsgsgtdftltisslepedfavyycqgrskwptfagggtkvek 125
|||||
Qy 63 GSGSGTDFLTISNLEPEDFAVYCCQPSDW-VTFGGTKVEIK 105
|||||

RESULT 8
ENTRY      S40344 *type complete
TITLE      Ig kappa light chain (VJ) - human
ORGANISM   *formal_name Homo sapiens *common_name man
DATE       19-May-1994 *sequence_revision 26-May-1995 *text_change
16-Aug-1996
ACCESSIONS S40344
REFERENCE   Klein, R.; Jaenichen, R.; Zachau, H.G.
              Eur. J. Immunol. (1993) 23:3248-3271
              Expressed human immunoglobulin chi genes and their
              hypermutation.
*accession S40344
**status    preliminary: translation not shown
**molecule_type mRNA
**residues  1-125 *label KLE
**cross-references EMBL:X72454
CLASSIFICATION *superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS       heterotetramer: immunoglobulin
SUMMARY        #length 125 *molecular-weight 13668 #checksum 4079

Query Match      88.8%; Score 655; DB 7; Length 125;
Best Local Similarity 92.2%; Pred. No. 2.61e-66;
Matches 94; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Db 24 ltqspatlsppgeratlsctasqsvsyawyyqkspqprlliyasratgiparfs 83
|||||
Qy 3 LTQSPATLSLSPGERATLSCTASQSVNKYLAWYQCKPQAPPLIYDASNPAITGIPAPFS 62
|||||

Db 84 gsgsgtdftltisslepedfavyycqgrskwptfagggtkvek 125
|||||
Qy 63 GSGSGTDFLTISNLEPEDFAVYCCQPSDW-VTFGGTKVEIK 103
|||||

RESULT 9
ENTRY      S29627 *type complete
TITLE      Ig kappa chain V region - human
ORGANISM   *formal_name Homo sapiens *common_name man
DATE       06-Jan-1995 *sequence_revision 06-Jan-1995 *text_change
25-Oct-1995
ACCESSIONS S34110; S29627
REFERENCE   Walls, M.A.; Hsiao, K.; Harris, L.J.
              Nucleic Acids Res. (1993) 21:2221-2229
              Vectors for the expression of PCR-amplified immunoglobulin
              variable domains with human constant regions.
*accession S34110
**status    preliminary: nucleic acid sequence not shown;
              translation not shown
**molecule_type DNA
**residues  1-129 *label WA2
**cross-references EMBL:Z17330
**note       the nucleotide sequence was submitted to the EMBL Data
              Library, October 1992

GENETICS      17/1
*introns      #superfamily immunoglobulin V region: immunoglobulin homology
CLASSIFICATION heterotetramer: immunoglobulin
KEYWORDS       #length 129 *molecular-weight 13910 #checksum 5282
SUMMARY

Query Match      87.9%; Score 649; DB 7; Length 129;
Best Local Similarity 89.6%; Pred. No. 1.54e-65;
Matches 95; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

Db 24 ltqspatlsppgeratlsctasqsvsyawyyqkspqprlliyasratgiparfs 83
|||||
Qy 3 LTQSPATLSLSPGERATLSCTASQSVNKYLAWYQCKPQAPPLIYDASNPAITGIPAPFS 62
|||||

Db 84 gsgsgtdftltisslepedfavyycqgrskwptfagggtkvek 129
|||||
Qy 63 GSGSGTDFLTISNLEPEDFAVYCCQPSDW-VTFGGTKVEIK 105
|||||

RESULT 10
ENTRY      S57444 *type fragment
TITLE      IgM light chain V-J region - human (fragment)
ORGANISM   *formal_name Homo sapiens *common_name man
DATE       10-Oct-1995 *sequence_revision 17-Nov-1995 *text_change
09-May-1997
ACCESSIONS S57444
REFERENCE   S57408

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Paterson, G.; Willson, G.; Kennedy, G.E.; Willison, H.J.
 submitted to the EMBL Data Library, June 1995
 Analysis of anti-GM1 ganglioside IgM antibodies cloned from
 motor neuropathy patients demonstrates diverse variable
 region gene usage with extensive somatic mutation.

#accession S57444
#status preliminary
#molecule_type mRNA
#residues 1-107 #label PAT
#cross-references EMBL:X87898
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 107 #checksum 7400

Query Match 86.9%; Score 641; DB 7; Length 107;
 Best Local Similarity 87.5%; Pred. No. 1.64e-64;
 Matches 91; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Db 4 ltqspatlslpgeratlscrasqsvstylaayqkpgqspsllydasnraagaiaarfs 63
 QY 3 LTQSPATLSLSPGERATLSCRASQSVNKYLAAYQKPGQAPRLIYDASNRATGIPARFS 62
 Db 64 gsgsgtdftltisslepedfavyvqgqrsnwpptfgdgtnvesk 107
 QY 63 GSGSGTDFTLTISNLEPEDFAVYVCQQRSDWV-TFGGTRKVEIK 105

RESULT 11
ENTRY H44151 #type fragment
TITLE Ig kappa chain V region (JM-15) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 16-Aug-1996

ACCESSIONS H44151
REFERENCE A44151
authors Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.;
 Graff, R.; DeGraw, J.; Pyatt, J.; Lapolla, R.; Burton,
 D.R.; Lerner, R.A.; Thornton, G.B.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179
#title Human combinatorial antibody libraries to hepatitis B surface
 antigen.

#accession H44151
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-108 #label ZEB
#note nucleotide translation not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 108 #checksum 1576

Query Match 85.5%; Score 631; DB 7; Length 108;
 Best Local Similarity 86.8%; Pred. No. 3.14e-63;
 Matches 92; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Db 1 aeltspatlslpgeratlscrasqsvssylaayqkpgqaprllygassratgipd 60
 QY 1 AELTSPATLSLSPGERATLSCRASQSVNK-YLAAYQKPGQAPRLIYDASNRATGIPA 59

Db 61 rfsgsgtdftltisrlepedfavyvqgqspptfggatkvelk 106
 QY 60 RFGSGSGTDFTLTISNLEPEDFAVYVCQQRSDWVTFGGTRKVEIK 105

RESULT 12
ENTRY K3HUVG #type complete
TITLE Ig kappa chain precursor V-III region (Vg) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 06-Sep-1996

ACCESSIONS A01900
REFERENCE A93549
authors Pech, M.; Zachau, H.G.
#journal Nucleic Acids Res. (1984) 12:9229-9236
#title Immunoglobulin genes of different subgroups are

interdigitated within the V-K locus.
#cross-references MIM:85087932
#accession A01900
#molecule_type DNA
#residues 1-115 #label PEC
#note the sequence was determined from the germline gene

GENETICS GDB:IGKV3
#gene GDB:136266
#introns 17/1
COMPLEX An immunoglobulin heterotetramer subunit consists of two
 identical light (kappa or lambda) and two identical heavy
 (alpha, delta, epsilon, gamma, or mu) chains usually
 stabilized by interchain disulfide bonds. In some cases,
 such as IgA and IgM, the subunits associate into larger
 oligomers.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE #domain signal sequence #status predicted #label SIG\
 1-20 #product Ig kappa chain V-III region (Vg) #status
 21-115 Predicted #label MAT\
 21-43 #region framework 1\
 44-54 #region complementarity-determining 1\
 55-69 #region framework 2\
 70-76 #region complementarity-determining 2\
 77-108 #region framework 3\
 109-115 #region complementarity-determining 3\
 43-108 #disulfide_bonds #status predicted
SUMMARY #length 115 #molecular_weight 12575 #checksum 8230

Query Match 84.8%; Score 626; DB 2; Length 115;
 Best Local Similarity 95.6%; Pred. No. 1.37e-62;
 Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlslpgeratlscrasqsvssylaayqkpgqaprllydasnratgiparfs 83
 QY 3 LTQSPATLSLSPGERATLSCRASQSVNKYLAAYQKPGQAPRLIYDASNRATGIPARFS 62
 Db 84 gsgsgtdftltisslepedfavyvqgqrsnw 114
 QY 63 GSGSGTDFTLTISNLEPEDFAVYVCQQRSDW 93

RESULT 13
ENTRY S40362 #type complete
TITLE Ig kappa chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 16-Aug-1996

ACCESSIONS S40362
REFERENCE S40312
authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their
 hypermutation.

#accession S40362
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-117 #label KLE
#cross-references EMBL:X72472
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 117 #molecular_weight 12613 #checksum 8309

Query Match 84.8%; Score 626; DB 7; Length 117;
 Best Local Similarity 84.6%; Pred. No. 1.37e-62;
 Matches 88; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 14 mtqspatlslpgeratlscrasqsvssnlaayqkpgqaprllygastatgiparfs 73
 QY 3 LTQSPATLSLSPGERATLSCRASQSVNKYLAAYQKPGQAPRLIYDASNRATGIPARFS 62

Db 74 usgsqtdftltlisslepedfavyycqqrnsdwvifgqgtkveik 117
 QY 63 GSGSGTDTLTISLSPGEPATLSGPASQSVN-KYLAWYQKPGQAPPELLIYDASNFAIGIPAPF 105

RESULT 14
 ENTRY S11697 #type complete
 TITLE Ig kappa chain precursor V-III region - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 ACCESSIONS S11697
 REFERENCE S11697
 #authors Pech, M.; Smola, H.; Pohlenz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
 #journal J. Mol. Biol. (1995) 183:291-299
 #title A large section of the gene locus encoding human immunoglobulin variable regions of the kappa type is duplicated.
 #cross-references MUID:85264787
 #accession S11697 preliminary; nucleic acid sequence not shown; translation not shown
 #status
 ##molecule_type DNA
 ##residues 1-115 ##label PEC
 ##cross-references EMBL:X17264
 ##note the nucleotide sequence was submitted to the EMBL Data Library, December 1989

GENETICS
 #introns 17/1
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 SUMMARY #length 115 #molecular_weight 12599 #checksum 7620

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 Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

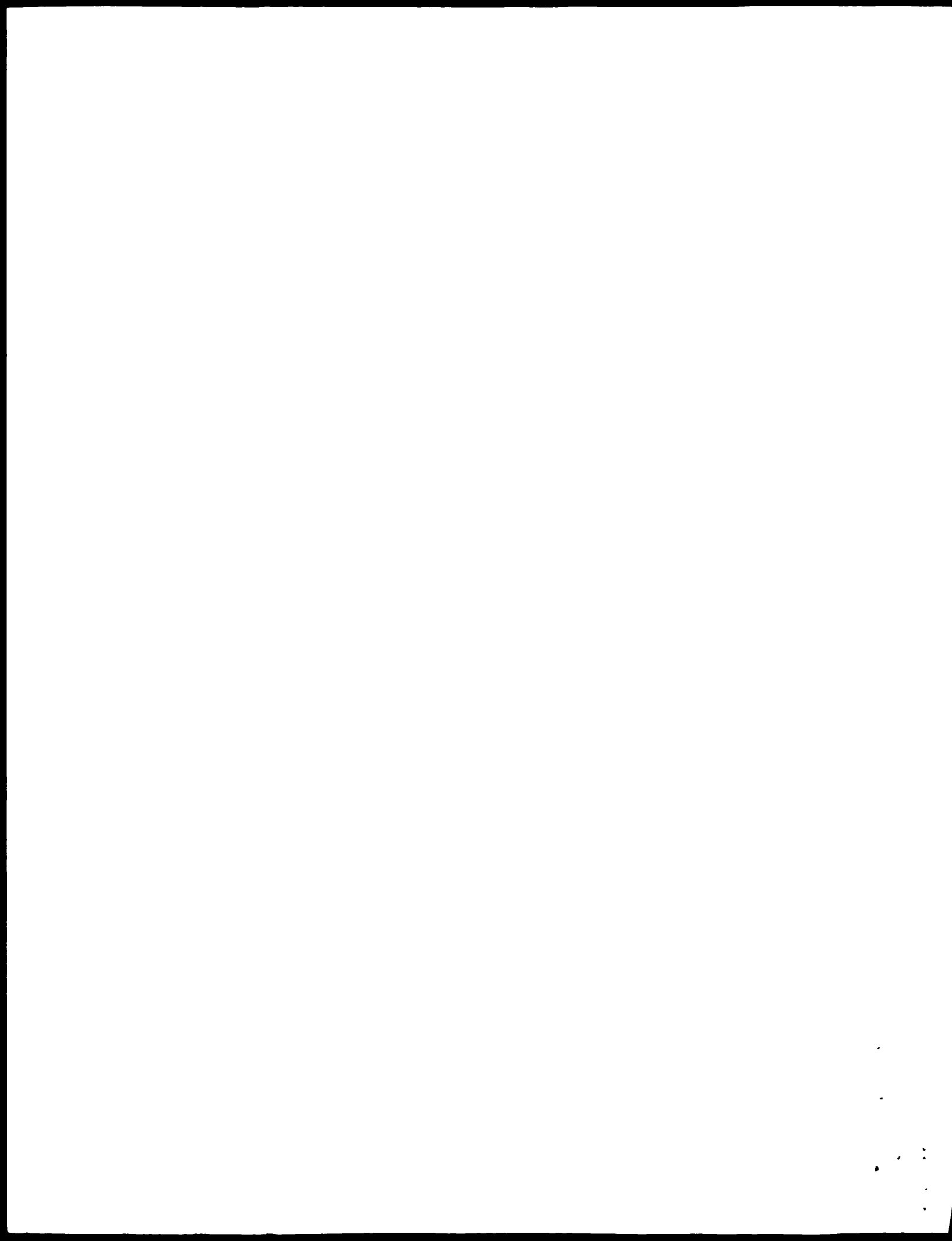
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 Db 84 qsgqtdftltlisslepedfavyycqqrnsdw 114
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RESULT 15
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 TITLE Ig kappa chain V-III region (Jh) - human (fragment)
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
 ACCESSIONS E30609
 REFERENCE A30601
 #authors Goni, F. P.; Chen, P. P.; McGinnis, D.; Arjonilla, M. L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, R.
 #journal J. Immunol. (1989) 142:3158-3163
 #title Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.
 #cross-references MUID:89215279
 #accession E30609 preliminary
 #status
 ##molecule_type protein
 ##residues 1-108 ##label GON
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 SUMMARY #length 108 #checksum 199

Query Match 83.6%; Score 617; DB 7; Length 108;
 Best Local Similarity 84.6%; Pred. No. 1.95e-61;
 Matches 88; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

Db 4 ltqspatlsqperatlsqasqvsnylawyqkqpgqaprllydasnratgiparfs 53
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 Db 64 sgsqsgtdftltlisslepedfavyycqqrnsdwvifgqgtkveik 107
 QY 62 SSGSGTDTLTISLSPGEPATLSGPASQSVN-KYLAWYQKPGQAPPELLIYDASNFAIGIPAPF 105

Search completed: Tue Feb 24 07:19:49 1998
 Job time : 12 secs.



WARNING
 ***** (TM)

Release 2.12 John F. Collins, BioComputing Research Unit
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 MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Feb 24 07:46:01 1998: Maspar time 3 01 Seconds
 Tabular output not generated. 177.704 Million cell updates/sec

Title: >US-08-844-215-9
 Description: (1-105) from US08844215.pep
 Perfect Score: 738
 Sequence: 1 AELTQSPATLSLSPGERATL.....YQQRSDWVTFGGTKVEIK 105

Scoring table: PAM 150
 Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-issued
 1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:58 10:59
 10:PT92 11:PT93 12:PT94 13:PT95 14:PT96

Statistics: Mean 27.520 Variance 149.406 scale 0.184

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description	Pred. No.
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2	620	84	0	115	7	US-08-053- Sequence 181, Applicat	1 30e-38
3	616	83	5	109	13	PCT-US95-0 Sequence 147, Applicat	2 65e-38
4	615	83	5	109	7	US-08-276- Sequence 147, Applicat	2 65e-38
5	608	82	4	111	7	PCT-US95-0 Sequence 149, Applicat	1 10e-37
6	609	82	4	111	13	PCT-US95-0 Sequence 149, Applicat	1 10e-37
7	606	82	1	107	13	PCT-US95-0 Sequence 90, Applicat	1 56e-37
8	606	82	1	107	7	US-08-276- Sequence 86, Applicat	1 87e-37
9	605	82	0	108	7	US-08-276- Sequence 86, Applicat	1 87e-37
10	605	82	0	108	13	PCT-US95-0 Sequence 86, Applicat	1 87e-37
11	600	81	3	108	6	US-08-477- Sequence 86, Applicat	4 54e-37
12	600	81	3	108	6	US-08-634- Sequence 86, Applicat	4 54e-37
13	600	81	3	108	7	US-08-474- Sequence 86, Applicat	4 54e-37
14	600	81	3	108	7	US-08-487- Sequence 86, Applicat	4 54e-37
15	594	80	5	107	13	PCT-US95-0 Sequence 87, Applicat	1 32e-36
16	594	80	5	107	7	US-08-276- Sequence 87, Applicat	1 32e-36
17	594	80	5	108	13	PCT-US95-0 Sequence 87, Applicat	1 32e-36
18	594	80	5	108	7	US-08-276- Sequence 87, Applicat	1 32e-36
19	593	80	4	104	13	PCT-US95-0 Sequence 99, Applicat	1 32e-36
20	593	80	4	104	7	US-08-276- Sequence 100, Applicat	1 32e-36
21	591	80	1	104	11	PCT-US95-0 Sequence 100, Applicat	1 32e-36
22	585	79	3	108	7	US-08-276- Sequence 110, Applicat	6 44e-36

23	585	79	3	108	13	PCT-US95-0 Sequence 110, Applicat	6 44e-36
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27	581	79	7	107	7	US-08-474- Sequence 57, Applicat	1 32e-35
28	581	79	7	107	7	US-08-474- Sequence 57, Applicat	1 32e-35
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32	581	78	7	107	7	US-08-487- Sequence 57, Applicat	1 32e-35
33	566	76	7	104	13	PCT-US95-0 Sequence 94, Applicat	1 88e-34
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36	564	76	4	108	13	PCT-US95-0 Sequence 96, Applicat	2 68e-34
37	563	76	3	112	13	PCT-US95-0 Sequence 151, Applicat	3 20e-34
38	563	76	3	112	7	US-09-053- Sequence 151, Applicat	3 20e-34
39	562	76	2	116	7	US-08-276- Sequence 183, Applicat	7 76e-34
40	558	75	6	108	7	US-08-276- Sequence 88, Applicat	7 76e-34
41	558	75	6	108	13	PCT-US95-0 Sequence 88, Applicat	7 76e-34
42	546	74	0	107	11	PCT-US95-0 Sequence 18, Applicat	6 48e-33
43	543	73	6	107	6	US-07-634- Sequence 34, Applicat	1 10e-32
44	543	73	6	107	6	US-08-477- Sequence 34, Applicat	1 10e-32
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ALIGNMENTS

RESULT 1
 ID US-08-053-131-179 STANDARD: PRT: 115 AA.
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DT 01-JAN-1900

DE Sequence 179, Application US/08053131.

XX

Sequence 179, Application US/08053131
 Patent No. 5661016
 GENERAL INFORMATION:

APPLICANT: Lonberg, Nils
 APPLICANT: Kay, Robert M.
 TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
 TITLE OF INVENTION: Producing Heterologous Antibodies
 NUMBER OF SEQUENCES: 197
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 200
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/053,131
 FILING DATE: 26-Apr-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,860
 FILING DATE: 16-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/810,279
 FILING DATE: 17-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/953,408
 FILING DATE: 18-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOC# NUMBER: 14643-9-3

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CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 179:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 115 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 115 AA: 12575 MW; 71214 CN;
SQ
Query Match 84.8%; Score 626; DB 7; Length 115;
Best Local Similarity 95.6%; Pred. No. 4.48e-39;
Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 24 LTQSPATLSLSPGERATLSRASQSVSYLAWYQCKPGQAPRLLIYDASNATGIPARFS 83
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ID US-08-053-131-181 STANDARD: PRT: 115 AA.
XX
AC xxxxxx
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DT 01-JAN-1900
XX
DE Sequence 181, Application US/08053131.
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CC
CC Sequence 181, Application US/08053131
CC Patent No. 5661016
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourile and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
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CC PRIOR APPLICATION DATA:
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CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-Q-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC
CC INFORMATION FOR SEQ ID NO: 181:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 115 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 115 AA: 12599 MW; 70085 CN;
SQ
Query Match 84.0%; Score 620; DB 7; Length 115;
Best Local Similarity 93.4%; Pred. No. 1.30e-38;
Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db 24 LTQSPATLSLSPGERATLSRASQSVSYLAWYQCKPGQAPRLLIYDASNATGIPARFS 83
QY 3 LTQSPATLSLSPGERATLSRASQSVSYLAWYQCKPGQAPRLLIYDASNATGIPARFS 62
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QY 63 GSGSGTDFTLTISSLEPEDFAVYQCQRSDW 93
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AC xxxxxx
XX
DT 01-JAN-1900
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DE Sequence 147, Application PC/TUS9508743.
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CC
CC Sequence 147, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
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CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
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CC MOLECULE TYPE: protein
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Best Local Similarity 84.9%; Pred. No. 2.65e-38;
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Db 62 RFSGSGTDFTLTISSLEPEDFAVYQCQRSDW 107
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DT 01-JAN-1900
 XX Sequence 147, Application US/08276852.
 DE Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1 0, Version #1 25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCR1452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 147:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 109 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 109 AA; 11779 MW; 65550 CN;

 Query Match 83.5%; Score 616; DB 7; Length 109;
 Best Local Similarity 84.9%; Pred No 2 65e-3a;
 Matches 90; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

 Db 2 AELTOSPTLSLSPGERIVVSCRASQSVSSNYLAWYQKFGQAPRLIYQASNRATGIPD 61
 QY 1 AELTOSPTLSLSPGERATLSQASQSVN-KYLAWYQKFGQAPRLIYQASNRATGIPA 59
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 ID US-08-276-852-149 STANDARD: PRT: 111 AA.
 XX xxxxxx
 XX 01-JAN-1900
 DE Sequence 149, Application US/08276852.
 DT

XX Sequence 149, Application US/08276852
 CC Patent No. 5652138
 CC GENERAL INFORMATION:
 CC APPLICANT: Burton, Dennis R
 CC APPLICANT: Barbas, Carlos F
 CC APPLICANT: Lerner, Richard A
 CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: The Scripps Research Institute, Office of
 CC ADDRESSEE: Patent Counsel
 CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
 CC CITY: La Jolla
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
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 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCR1452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 149:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 111 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 111 AA; 11956 MW; 63169 CN;

 Query Match 82.4%; Score 608; DB 7; Length 111;
 Best Local Similarity 83.0%; Pred. No. 1.10e-37;
 Matches 88; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

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 QY 1 AELTOSPTLSLSPGERATLSQASQSVN-KYLAWYQKFGQAPRLIYQASNRATGIPA 59
 Db 62 RFGSGSGTDTLTISLPEDEFAVYVQYQYSGSGTGGTKVEIK 107
 QY 60 RFGSGSGTDTLTISLPEDEFAVYVQYQYSGSGTGGTKVEIK 105

 RESULT 5
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 XX xxxxxx
 XX 01-JAN-1900
 DE Sequence 149, Application PC/TUS9508743.
 CC Sequence 149, Application PC/TUS9508743
 CC GENERAL INFORMATION:

CC APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 149:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 111 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 111 AA: 11956 MW: 63169 CN:
CC
CC Query Match 82.1%; Score 606; DB 13; Length 111;
CC Best Local Similarity 83.0%; Pred. No. 1.10e-37;
CC Matches 88; Conservative 7; Mismatches 10; Indels 1; Gaps 1;
DB 2 AELTQSPGTLSPGPRATISCRASQSVNSGYLAWYQKPGQAPRLIYGASTPATDIPD 61
QY 1 AELTQSPATLSLSPGPRATISCRASQSVNK-YLAWYQKPGQAPRLIYDASNRTATGIPAR 59
DB 62 RFGSGSGAGFTLTISNLEPDEFVAVYCCQQRSDWMTFPGGKTKEIK 107
QY 60 RFGSGSGDTFTLTISNLEPDEFVAVYCCQQRSDWMTFPGGKTKEIK 105
RESULT 7
ID PCT-US95-08743-90 STANDARD; PRT; 107 AA.
XX XXXXXX
XX 01-JAN-1900
DE Sequence 90, Application PC/TUS9508743.
CC Sequence 90, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 90:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11705 MW: 62938 CN:
CC
CC Query Match 82.1%; Score 606; DB 13; Length 107;
CC Best Local Similarity 82.1%; Pred. No. 1.56e-37;
CC Matches 87; Conservative 10; Mismatches 7; Indels 2; Gaps 2;

DB 1 ELTQSPGTLSPGPRATISCRASQSVNSGYLAWYQKPGQAPRLIYGSSTRTGIPDR 60
QY 2 ELTQSPATLSLSPGPRATISCRASQSV-NKYLAWYQKPGQAPRLIYDASNRTATGIPAR 60
DB 61 FSGSGSGDTFTLTISNLEPDEFVAVYCCQHYGNSVYTFGGTKLEIK 106
QY 61 FSGSGSGDTFTLTISNLEPDEFVAVYCCQQRSDWMTFPGGKTKEIK 105
RESULT 8
ID US-08-276-852-90 STANDARD; PRT; 107 AA.
XX XXXXXX
XX 01-JAN-1900
DE Sequence 90, Application US/08276852.
XX Sequence 90, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC STREET: 10556 No. 5852138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop IPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCP1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 90:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 107 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 107 AA: 11705 MW: 62938 CN:
CC
CC Query Match 82.1%; Score 606; DB 7; Length 107;
CC Best Local Similarity 82.1%; Pred. No. 1.56e-37;
CC Matches 87; Conservative 10; Mismatches 7; Indels 2; Gaps 2;

QY 2 ELTQSPATLSLSPGERATLSRQASQSV-NKYLAWYQKPGCAPPLLIYDASNATGIPAP 60
Db 61 FSGSGGTDFLTISRLEPEDFAVYQCHYQNSVYTFGGQTKLEIK 106
QY 61 FSGSGGTDFLTISRLEPEDFAVYQCHYQNSVYTFGGQTKVEIK 105

RESULT 9
ID US-08-276-852-86 STANDARD: PRT: 108 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 86, Application US/08276852
XX
CC Sequence 86, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10655 No. 5652138th Torrey Pines Road, Suite 220,
CC STREET: Mail Drop TPC8
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/129,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCPI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11769 MW: 65957 CN;

Query Match 82.0% Score 605; DB 7; Length 108;
Best Local Similarity 86.0%; Pred. No. 1,87e-37;
Matches 92, Conservative 3, Mismatches 8, Indels 4, Gaps 3.

Db 1 ELTQSPATLSLSPGERATLSRQASQSV-NKYLAWYQKPGCAPPLLIYDASNATGIPAP 60
QY 2 ELTQSPATLSLSPGERATLSRQASQSV-NKYLAWYQKPGCAPPLLIYDASNATGIPAP 60
Db 61 FSGSGGTDFLTISRLEPEDFAVYQCHYQNSVYTFGGQTKVEIK 106

QY 61 FSGSGGTDFLTISRLEPEDFAVYQCHYQNSVYTFGGQTKVEIK 105

RESULT 10
ID PCT-US95-08743-86 STANDARD: PRT: 108 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 86, Application PC/TUS9508743.
XX
CC Sequence 86, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EP0)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA: 11769 MW: 65957 CN;

Query Match 82.0% Score 605; DB 12; Length 108;
Best Local Similarity 86.0%; Pred. No. 1,87e-37;
Matches 92, Conservative 3, Mismatches 9, Indels 4, Gaps 3.

Db 1 ELTQSPATLSLSPGERATLSRQASQSV-NKYLAWYQKPGCAPPLLIYDASNATGIPAP 60
QY 2 ELTQSPATLSLSPGERATLSRQASQSV-NKYLAWYQKPGCAPPLLIYDASNATGIPAP 60
Db 61 FSGSGGTDFLTISRLEPEDFAVYQCHYQNSVYTFGGQTKVEIK 106
QY 61 FSGSGGTDFLTISRLEPEDFAVYQCHYQNSVYTFGGQTKVEIK 105

RESULT 11
ID US-08-477-728-86 STANDARD: PRT: 108 AA.
XX xxxxxx
XX 01-JAN-1900
DE Sequence 86, Application US/08477728.
XX
CC Sequence 86, Application US/08477728
CC Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Gary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: Palo Alto
CC STATE: California

CC COUNTRY: US
 CC ZIP: 94111
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/477,728
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002600
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 86:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 108 AA; 11590 MW; 64079 CN;

Query Match 81.3%; Score 600; DB 6; Length 108;
 Best Local Similarity 84.8%; Pred. No. 4.54e-37;
 Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Db 4 LTQSPGTLSPGERATLSRLEPEPEFAVYVQYQSGLSGRTEFGGQTKVEIK 108
 QY 3 LTQSPATLSLSPGERATLSRLEPEPEFAVYVQYQSGLSGRTEFGGQTKVEIK 108
 Db 64 SGSSGSGTDTLTISRLPEPEFAVYVQYQSGLSGRTEFGGQTKVEIK 108
 QY 62 SGSSGSGTDTLTISRLPEPEFAVYVQYQSGLSGRTEFGGQTKVEIK 105

RESULT 12
 ID US-07-634-278-86 STANDARD; PRT; 108 AA.

XX xxxxxx
 XX 01-JAN-1900
 DE Sequence 86, Application US/07634278.
 XX Sequence 86, Application US/07634278.
 CC Patent No. 5530101
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: CO. Man Sung
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: LANDOLFI, Nicholas F.
 CC APPLICANT: COELING, Kathleen L.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/634,278
 CC FILING DATE: 19-DEC-1990
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002600
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 86:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 108 AA; 11590 MW; 64079 CN;

Query Match 81.3%; Score 600; DB 6; Length 108;
 Best Local Similarity 84.8%; Pred. No. 4.54e-37;
 Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Ub 4 LTQSPGTLSPGERATLSRLEPEPEFAVYVQYQSGLSGRTEFGGQTKVEIK 108
 QY 3 LTQSPATLSLSPGERATLSRLEPEPEFAVYVQYQSGLSGRTEFGGQTKVEIK 108
 Db 64 SGSSGSGTDTLTISRLPEPEFAVYVQYQSGLSGRTEFGGQTKVEIK 108
 QY 62 SGSSGSGTDTLTISRLPEPEFAVYVQYQSGLSGRTEFGGQTKVEIK 105

RESULT 13
 ID US-08-474-040-86 STANDARD; PRT; 108 AA.

XX xxxxxx
 XX 01-JAN-1900
 DE Sequence 86, Application US/08474040.
 XX Sequence 86, Application US/08474040.
 CC Patent No. 5693761
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: CO. Man Sung
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: LANDOLFI, Nicholas F.
 CC APPLICANT: COELING, Kathleen L.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113

CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/474,040
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002400
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 81.3%; Score 600; DB 7: Length 108;
Best Local Similarity 84.8%; Pred. No. 4.54e-37;
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Db 4 LTQSPGTLSPGEPATLSCPASQSVSSGYLGWYQKPGQAPPLIYGASSRATGIPDPF 63
QY 3 LTQSPATLSLSPGEPATLSCPASQSVNK-YLAWYQKPGQAPPLIYDASNRATGIPARF 61
Db 64 SSGSGTDFTLTISLPEDEFAVYQCYQYSLGHTFGGKVEIK 108
QY 62 SSGSGTDFTLTISLPEDEFAVYQCYQYSLGHTFGGKVEIK 105

RESULT 14
ID US-08-487-200-86 STANDARD: PRT: 108 AA
XX
AC
XX
DT 01-JAN-1900

Sequence 86, Application US/08487200.
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: BELINGH, Kathleen L.

CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/487,200
CC FILING DATE: 7-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002610
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 81.3%; Score 600; DB 7: Length 108;
Best Local Similarity 84.8%; Pred. No. 4.54e-37;
Matches 89; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Db 4 LTQSPGTLSPGEPATLSCPASQSVSSGYLGWYQKPGQAPPLIYGASSRATGIPDPF 63
QY 3 LTQSPATLSLSPGEPATLSCPASQSVNK-YLAWYQKPGQAPPLIYDASNRATGIPARF 61
Db 64 SSGSGTDFTLTISLPEDEFAVYQCYQYSLGHTFGGKVEIK 108
QY 62 SSGSGTDFTLTISLPEDEFAVYQCYQYSLGHTFGGKVEIK 105

RESULT 15
ID PCT-US95-08743-87 STANDARD: PRT: 107 AA.
XX
AC
XX
DT 01-JAN-1900

Sequence 87, Application PCT/US9508743.
Sequence 87, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 CC NUMBER OF SEQUENCES: 170
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1 25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/08743
 CC FILING DATE: 11-JUL-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/276,852
 CC FILING DATE: 18-JUL-1994
 CC INFORMATION FOR SEQ ID NO: 87:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 107 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 107 AA; 11654 MW; 62438 CN;
 Query Match 80.5%; Score 594; DB 13; Length 107;
 Best Local Similarity 83.0%; Pred. No. 1.32e-36;
 Matches 88; Conservative 8; Mismatches 8; Indels 2; Gaps 2;
 Db 1 ELTQSPGTLSPGPRATLSGRASQSVSNVYLAWYQQQPGQAPGAPLLIYGASNPATGIPDR 60
 QY 1 ELTQSPATLSLSPGPRATLSGRASQSV-NKYLAWYQQQPGQAPGAPLLIYDASNPATGIPAP 60
 Db 61 FSGSGGTAFITLTISLQPEDVAIYQQVHSSPYTFGGTKLEIK 106
 QY 61 FSGSGGTDFLTITISNLEPEDFAVYVCOQ-RSDWVTFGGTKVEIK 105

Search completed: Tue Feb 24 07:46:22 1998
 Job time : 21 secs.

W P E R E H

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:20:07 1998; MasPar time 5.74 Seconds
Tabular output not generated. 216,418 Million cell updates/sec
Title: >US-08-844-215-9
Description: (1-105) from US08844215.pgp
Perfect Score: 738
Sequence: 1 AELTUSPAILSLSPGPATL.....YCGPSPDWVFGGKVKVIR 105

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13889129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 30.157; Variance 177.084; scale 0.170

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES						
Result No	Score	Query Match	Length	DB	ID	Description
1	549	87.9	349	2	R12128	1B1 IgG aberrant light
2	549	87.9	401	2	R12129	ORF 1 of IgG light chain
3	549	87.9	414	2	R12128	1B1 IgG aberrant light
4	549	87.9	414	2	R13117	1B1 IgG aberrant light
5	525	84.8	115	7	R38648	Human V-kappa fragment
6	526	84.8	115	11	R62928	Human V-kappa vK65.3
7	526	84.8	120	20	W03945	DNA fragment vK65.3
8	520	84.0	115	7	R38648	Human V-kappa fragment
9	520	84.0	115	11	R62928	Human V-kappa vK65.5
10	520	84.0	115	20	W03947	DNA fragment vK65.5
11	516	83.5	109	10	R54275	Anti-HIV gp41 immunog
12	516	83.5	109	19	W01320	VL of Fab, DL 41 19,
13	511	82.8	109	10	R56286	Light chain of Abn al
14	508	82.4	111	19	W01322	VL of Fab, GL 41 1, b
15	508	82.4	111	10	R54277	Anti-HIV gp41 immunog
16	505	82.1	107	22	W08949	Kappa light chain var
17	506	82.1	107	10	R54311	Anti-HIV gp120 immuno
18	505	82.1	107	19	W01269	VL region of HIV neut
19	505	82.0	108	10	R54307	Anti-HIV gp120 immuno
20	505	82.0	108	19	W01265	VL region of HIV neut

21	604	81.8	107	7	R38593	Human lambda light ch	1.76e-33
22	602	81.4	129	7	R38573	PI05VK-PI05V	2.44e-33
23	602	81.5	129	7	R42866	PI05 rearranged varia	2.44e-33
24	599	81.2	129	7	R38672	W325-JK2	3.99e-33
25	595	80.8	127	22	W09446	Fappa light chain var	4.52e-33
26	594	80.5	107	19	W01268	VL region of HIV neut	9.04e-33
27	594	80.5	107	10	R54308	Anti-HIV gp120 immuno	9.04e-33
28	594	80.5	108	19	W01278	VI region of HIV neut	9.04e-33
29	594	80.5	108	9	R54316	Anti-HIV gp120 immuno	9.04e-33
30	593	80.4	104	9	R54317	Anti-HIV gp120 immuno	1.06e-32
31	593	80.4	104	19	W01279	VL region of HIV neut	1.06e-32
32	591	80.1	109	9	R50217	HSV glycoprotein F b1	1.48e-32
33	590	79.9	107	22	W08948	Kappa light chain var	1.74e-32
34	585	79.3	108	19	W01289	VL region of HIV neut	3.93e-32
35	585	79.3	112	2	P81245	Anti-pseudomonas aeru	3.93e-32
36	585	79.3	128	1	P41001	Anti-p aeruginosa st	3.93e-32
37	585	79.3	234	0	R52051	human anti-IgF MAT li	3.93e-32
38	583	79.0	109	9	R50218	HSV glycoprotein F b1	5.45e-32
39	581	78.7	107	5	R25729	Humanised VL region o	7.55e-32
40	578	78.3	109	10	R54263	Anti-HIV gp120 immuno	1.23e-31
41	575	77.9	134	20	W11155	Anti-lung tumour anti	2.01e-31
42	574	77.8	107	7	R37612	hIL2R Ab L chain V re	2.37e-31
43	573	77.6	127	9	R50192	LigHC chain variable	2.79e-31
44	573	77.6	127	9	R50187	light chain variable	2.79e-31
45	571	77.4	127	9	R50191	light chain variable	3.86e-31

ALIGNMENTS

RESULT 1
ID R12128 standard: Protein; 349 AA.
AC R12128:
DT 01-AUG-1991 (first entry)
DE 1B1 IgG aberrant light chain with duplicated variable region.
KW immunoglobulin G; light chain; variable region; duplication;
KW passive immunity; group B streptococci.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= leader peptide
FT /region 18..130
FT /label= variable region
FT /note= "L'V 1"
FT /region 131..243
FT /label= variable region
FT /note= "L'V 2"
FT /region 244..345
FT /label= constant region
FN W09105305-A.
PD 16-MAY-1991.
PP 06-NOV-1990; W06426.
PP 07-NOV-1989; US-432700.
PA (BRIM) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DP N-PSB; Q11878.
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Example 5, Fig 16, 104pp; English.
CC This sequence is deduced from the cDNA clone 4B9-VK15 and includes
CC the amino acid sequence beyond the first stop codon. The clone is
CC incomplete, starting from the 5' of the Arg initiator codon, but the
CC initial Met is given. Antibody molecules of the invention can
CC include one or two aberrant light chains containing a duplicated
CC variable region, to produce heavier antibodies. These heavier
CC antibodies were found to have higher avidity than antibodies with
CC just a single copy of the L'V region. The antibodies can be used to
CC treat disease, e.g. infection by Streptococcus agalactiae. They are
CC able to pass across the placenta.
CC See also Q11879 and Q11880.
SQ Sequence 349 AA;

```

Query Match      87.9%; Score 649; DB 2; Length 349;
Best Local Similarity 89.6%; Pred. No. 1,11e-36;
Matches 95; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

Dd 24 ltqspatlsppgeratlsccrasgvsylawyqkpgqagprplydasnratgiparfs 83
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 3 LTQSPATLSLSPGERATLSPPASQSVNKYLAWYQKPGQAPPLIYDASNRAITGIPARFS 62

Dd 84 gsgsgtdftltisslepedfavyvqchrdnwpqgafgggtkveik 129
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 63 GSGSGTDFTLTISNLEPEDFAVYVQQRSDW---VTFGGGTKEIK 105

RESULT 2
ID R12129 standard; Protein; 401 AA.
AC R12129;
DE 01-AUG-1991 (first entry)
KW immunoglobulin G; light chain; variable region; duplication;
KW passive immunity; group B streptococci.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 224..336
FT /label= "L'V region"
FT /note= "last 3 amino acids of leader and variable
region"
PN WO9106305-A.
PD 16-MAY-1991.
PF 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DR WPI: 91-163947/22.
DR N-PSDB; Q11879.
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Example 4; Fig 17; 104pp; English.
CC This sequence is derived from the nucleotide sequence encoding the
CC light chain variable region. The "x" residues represent nonsense
CC codons. The coding sequence has been translated in all 3 reading
CC frames (see also R12130 and R12131). The L'V region is duplicated
CC in so-called "aberrant" light chains (see Q11878), conferring
CC increased avidity on antibodies comprising such aberrant chains.
CC See also Q11880.
SQ Sequence 401 AA;

Query Match      87.9%; Score 649; DB 2; Length 401;
Best Local Similarity 89.6%; Pred. No. 1,11e-36;
Matches 95; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

Dd 230 ltqspatlsppgeratlsccrasgvsylawyqkpgqagprplydasnratgiparfs 289
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 3 LTQSPATLSLSPGERATLSPPASQSVNKYLAWYQKPGQAPPLIYDASNRAITGIPARFS 62

Dd 290 gsgsgtdftltisslepedfavyvqchrdnwpqgafgggtkveik 335
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 63 GSGSGTDFTLTISNLEPEDFAVYVQQRSDW---VTFGGGTKEIK 105

RESULT 3
ID R13018 standard; Protein; 414 AA.
AC R13018;
DE 01-AUG-1991 (first entry)
DE 1B1 IgG aberrant light chain with duplicated variable region.
KW immunoglobulin G; light chain; variable region; duplication;
KW passive immunity; group B streptococci.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= leader peptide
FT Region 18..130
FT /label= variable region
FT /note= "L'V 1"
FT Region 131..243
FT /label= variable region
FT /note= "L'V 2"
FT Region 244..345
FT /label= constant region
PN WO9106305-A.
PD 16-MAY-1991.
PF 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DR WPI: 91-163947/22.
DR N-PSDB; Q11878.

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FT /note= "L'V 1"
FT Region 131..243
FT /label= variable region
FT /note= "L'V 2"
FT Region 244..345
FT /label= constant region
PN WO9106305-A.
PD 16-MAY-1991.
PF 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DR WPI: 91-163947/22.
DR N-PSDB; Q11878.
PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
PT formed by duplicating esp. variable region of light chain of IgG
PT class
PS Example 5; Fig 16; 104pp; English.
CC This sequence is deduced from the cDNA clone 439-Vk15 and includes
CC the amino acid sequence beyond the first stop codon ("x" in the
CC sequence represents a nonsense codon). The clone is incomplete,
CC starting from the G of the AIG initiator codon, but the initial Met
CC is given. Antibody molecules of the invention can include one or two
CC aberrant light chains containing a duplicated variable region, to
CC produce heavier antibodies. These heavier antibodies were found to
CC have higher avidity than antibodies with just a single copy of the
CC L'V region. The antibodies can be used to treat disease, e.g.
CC infection by Streptococcus agalactiae. They are able to pass across
CC the placenta.
CC See also Q11879 and Q11880.
SQ Sequence 414 AA;

Query Match      87.9%; Score 649; DB 2; Length 414;
Best Local Similarity 89.6%; Pred. No. 1,11e-36;
Matches 95; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

Dd 24 ltqspatlsppgeratlsccrasgvsylawyqkpgqagprplydasnratgiparfs 83
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 3 LTQSPATLSLSPGERATLSPPASQSVNKYLAWYQKPGQAPPLIYDASNRAITGIPARFS 62

Dd 84 gsgsgtdftltisslepedfavyvqchrdnwpqgafgggtkveik 129
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 63 GSGSGTDFTLTISNLEPEDFAVYVQQRSDW---VTFGGGTKEIK 105

RESULT 4
ID R13111 standard; Protein; 414 AA.
AC R13111;
DE 10-MAR-1993 (revised)
DE 01-AUG-1991 (first entry)
DE 1B1 IgG aberrant light chain with duplicated variable region.
KW immunoglobulin G; light chain; variable region; duplication;
KW passive immunity; group B streptococci.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= leader peptide
FT Region 18..130
FT /label= variable region
FT /note= "L'V 1"
FT Region 131..243
FT /label= variable region
FT /note= "L'V 2"
FT Region 244..345
FT /label= constant region
PN WO9106305-A.
PD 16-MAY-1991.
PF 06-NOV-1990; U06426.
PR 07-NOV-1989; US-432700.
PA (BRIM ) BRISTOL-MYERS SQUIB.
PI Shuford WW, Harris LJ, Raff HV;
DR WPI: 91-163947/22.
DR N-PSDB; Q11878.

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PT *Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 PS Example 5; Fig 16; 104pp; English.
 CC This sequence is deduced from the cDNA clone 4R9-Vk15 and includes
 CC the amino acid sequence beyond the first stop codon ("x" in the
 CC sequence represents a nonsense codon). The clone is incomplete,
 CC starting from the G of the ATG initiator codon, but the initial Met
 CC is given. Antibody molecules of the invention can include one or two
 CC aberrant light chains containing a duplicated variable region, to
 CC produce heavier antibodies. These heavier antibodies were found to
 CC have higher avidity than antibodies with just a single copy of the
 CC L/V region. The antibodies can be used to treat disease, e.g.
 CC infection by Streptococcus agalactiae. They are able to pass across
 CC the placenta.
 CC See also Q11879 and Q11880.
 SQ Sequence 414 AA;

Query Match 87.9%; Score 649; DB 2; Length 414;
 Best Local Similarity 89.6%; Pred No. 1,11e-36;
 Matches 95; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

Db 24 ltqspatlsppgeratlsccrasqsvsylvayqkqpgqaprpillydasnratgiparfs 83
 ||||||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||||||||||

Qy 3 ltqspatlsppgeratlsccrasqsvsylvayqkqpgqaprpillydasnratgiparfs 62

Db 84 qsgsgtdftltisslepedfavyvccqrshw 129

||||||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||||||||||

Qy 63 GSGSGTDTLTISNLEPEDFAVYVCCQQRSDW---VTFGGGKVEIK 105

RESULT

ID R38648 standard; Protein: 115 AA.

DI 10-NOV-1993 (first entry)

DE Human V-kappa fragment encoded by clone vk65.3.

KW Immunoglobulin; light chain variable region; minilocus;

KW isotype switching; unrearranged functional V κ gene segment;

KW human light chain transgene.

OS Homo sapiens.

PN Kay RM, Lonberg N.

PD WPI: 93-214169/25.

PF 24-JUN-1993.

PR 17-DEC-1992; U10983.

PR 17-DEC-1991; US-810279.

PR 18-MAR-1992; US-853408.

PR 23-JUN-1992; US-904068.

PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N.

DR N-PSDB: Q44222.

PT transgenic non-human animals contg. immunoglobulin heavy chain

PT trans gene - used to produce useful antibodies by isotype

PT switching

PS Example 21; Fig 41; 196pp; English.

CC The V-kappa specific oligonucleotide Q50327 was used to probe a

CC human placental genomic DNA library cloned into lambdaEMBL3/SB6/77

CC DNA fragments containing V-kappa segments from positive phage

CC clones were subcloned into plasmid vectors. Variable gene segments

CC from the resulting clones were sequenced and functional clones were

CC selected on the basis of open reading frames, intact donor and

CC acceptor splice sites and intact recombination sequences. The

CC sequences obtained from four different plasmid clones were

CC designated p65.3, p65.5, p65.8 and p65.15 (see Q44222-Q4425,

CC respectively) and the amino acid sequences of the V-kappa regions

CC they encode were deduced.

SQ Sequence 115 AA;

Query Match

Best Local Similarity 84.8%; Score 626; DB 7; Length 115;

Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlsppgeratlsccrasqsvsylvayqkqpgqaprpillydasnratgiparfs 83
 ||||||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||||||||||

Qy 3 ltqspatlsppgeratlsccrasqsvsylvayqkqpgqaprpillydasnratgiparfs 62
 Db 84 qsgsgtdftltisslepedfavyvccqrshw 114
 ||||||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||||||||||

Qy 63 GSGSGTDTLTISNLEPEDFAVYVCCQQRSDW 93

RESULT

ID R62928 standard; Protein: 115 AA.

AC R62928;

DI 07-JUN-1995 (first entry)

DE Human V-kappa vk65.3 region.

KW Transgenic mouse; transgenic animal; antibody engineering;

KW variable region; light chain; minilocus transgene;

KW chimeric antibody.

OS Homo sapiens.

PN WO9425585-A.

PD 10-NOV-1994.

PF 25-APR-1994; U04580.

PR 26-APR-1993; US-053131.

PR 22-JUL-1993; US-026762.

PR 18-NOV-1993; US-155301.

PR 03-DEC-1993; US-161739.

PR 10-DEC-1993; US-165699.

PR 09-MAR-1994; US-209741.

PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N.

DR WPI: 94-358263/44.

DR N-PSDB: Q78852.

PT transgenic non-human animals producing heterologous or chimeric

PT antibodies - for binding a pre-determined human antigen with

PT increased affinity

PS Disclosure: Fig. 41; 296pp; English.

CC Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in

CC Q78852-Q78855, respectively) each contain a V-kappa gene segment

CC that can be used to form a complete human light chain minilocus

CC transgene for expression in a nonhuman transgenic animal for

CC heterologous antibody production. The deduced amino acid

CC sequences of the V-kappa coding regions are given in #62928 #62931.

SQ Sequence 115 AA;

Query Match 84.8%; Score 626; DB 11; Length 115;

Best Local Similarity 95.6%; Pred. No. 4.82e-35;

Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlsppgeratlsccrasqsvsylvayqkqpgqaprpillydasnratgiparfs 83
 ||||||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||||||||||

Qy 3 ltqspatlsppgeratlsccrasqsvsylvayqkqpgqaprpillydasnratgiparfs 62

Db 84 qsgsgtdftltisslepedfavyvccqrshw 114

||||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||||||||||

Qy 63 GSGSGTDTLTISNLEPEDFAVYVCCQQRSDW 93

RESULT

ID W03946 standard; Protein: 120 AA.

AC W03946;

DI 14-APR-1997 (first entry)

DE DNA fragment vk65.3 variable kappa chain protein product.

KW Variable; kappa chain; gene segment; human; RNA fragment; vk65.3;

KW unrearranged; light chain; minilocus; transgene; transgenic; mouse;

KW production; heterologous; antibody, gamma; immunoglobulin.

OS Homo sapiens.

PN US5545806-A.

PD 13-AUG-1996.

PF 29-AUG-1990; 574748.

PR 29-AUG-1990; US-574748.

PR 31-AUG-1990; US-575962.

PR 17-DEC-1991; US-810279.

PR 18-MAR-1992; US-853408.

PR 23-JUN-1992; US-904068.

PR 16-DEC-1992; US-908660.

PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N;
DR WPI: 96-383736/38;
DR N-PSDB: T37180.

PT Prod'n. of heterologous human immunoglobulin(s) - by immunising
PT transgenic mice

PS Example 21; Fig 41; 94pp; English.

CC The present sequence is the protein product of the variable kappa
CC chain gene segment containing human DNA fragment, vk65.3, which
CC was co-injected along with the human DNA fragments vk65.5, vk65.8
CC and vk65.15 into half day mouse embryo pronuclei, to generate an
CC unrearranged light chain minilocus transgene. The resulting
CC transgenic mice can be used for the production of heterologous
CC (i.e. human) antibodies against specific antigens, this comprises
CC immunising a mouse with a preselected antigen and collecting
CC antigen binding heterologous human gamma immunoglobulins.
SQ Sequence 120 AA;

Query Match 84.8%; Score 626; DB 20; Length 120;
Best Local Similarity 95.6%; Pred. No. 4 82e-35;
Matches 87; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 29 ltqspatlsppgeratlscrasqsvsyawyyqkpgqprlliydasnratgiparfs 88

QY 3 LTQSPATLSLSPGERATLSQSPASQSVNKYLAWYQKPGQAPPLLIYDASNRTATGIPARFS 62

Db 89 gsgsgtdftltisslepedfavyycqrsnw 119

QY 63 GSGSGTDFLTISNLEPEDFAVYCYQQRSDW 93

RESULT 8

ID R38649 standard; Protein; 115 AA

AC R38649;

DT 10-NOV-1993 (first entry)

DE Human V-kappa fragment encoded by clone vk65.5.

KW Immunoglobulin; light chain variable region; minilocus;

KW isotype switching; unrearranged functional V κ gene segment;

KW human light chain transgene.

OS Homo sapiens.

PN W0912227-A.

PD 24-JUN-1993.

PF 17-DEC-1992; U10983.

PR 17-DEC-1991; US-810279.

PR 18-MAR-1992; US-853408.

PR 23-JUN-1992; US-904068.

PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N;

DR WPI: 93-214169/26.

DR N-PSDB: Q44223.

PT Transgenic non-human animals contg. immunoglobulin heavy chain

PT trans gene - used to produce useful antibodies by isotype

PT switching

PS Example 21; Fig 42; 196pp; English.

CC The V-kappa specific oligonucleotide Q50327 was used to probe a
CC human placental genomic DNA library cloned into lambdaEMBL3/SP6/T7.

CC DNA fragments containing V-kappa segments from positive phage

CC clones were subcloned into plasmid vectors. Variable gene segments

CC from the resulting clones were sequenced and functional clones were

CC selected on the basis of open reading frames, intact donor and

CC acceptor splice sites and intact recombination sequences. The

CC sequences obtained from four different plasmid clones were

CC designated p65.3, p65.5, p65.8 and p65.15 (see Q44222-Q44225,

CC respectively) and the amino acid sequences of the V-kappa regions

CC they encode were deduced.

SQ Sequence 115 AA;

Query Match 84.0%; Score 620; DB 7; Length 115;

Best Local Similarity 93.4%; Pred. No. 1.29e-34;

Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlsppgeratlscrasqsvsyawyyqkpgqprlliydasnratgiparfs 83

QY 3 LTQSPATLSLSPGERATLSQSPASQSVNKYLAWYQKPGQAPPLLIYDASNRTATGIPARFS 62

Db 84 gsgsgtdftltisslepedfavyycqrsnw 114

QY 63 GSGSGTDFLTISNLEPEDFAVYCYQQRSDW 93

RESULT 9

ID R62929 standard; Protein; 115 AA.

AC R62929;

DT 07-JUN-1995 (first entry)

DE Human V-kappa vk65.5 region.

KW Transgenic mouse; transgenic animal; antibody engineering;

KW variable region; light chain; minilocus transgene;

KW chimeric antibody.

OS Homo sapiens.

PN W09425585-A.

PD 10-NOV-1994.

PF 25-APR-1994; U04580.

PP 26-APR-1993; US-053131.

PR 22-JUL-1993; US-096762.

PR 18-NOV-1993; US-155301.

PR 03-DEC-1993; US-161739.

PR 10-DEC-1993; US-165699.

PP 09-MAR-1994; US-209741.

PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N;

DR WPI: 94-358263/44.

DR N-PSDB: Q78853.

PT Transgenic non-human animals producing heterologous or chimeric

PT antibodies - for binding a pre-determined human antigen with

PT increased affinity

PS Disclosure: Fig 42; 246pp; English

CC Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in

CC Q78852-Q78855, respectively) each contain a V-kappa gene segment

CC that can be used to form a complete human light chain minilocus

CC transgene for expression in a nonhuman transgenic animal for

CC heterologous antibody production. The deduced amino acid

CC sequences of the V-kappa coding regions are given in P62928-P62931.

SQ Sequence 115 AA;

Query Match 84.0%; Score 620; DB 11; Length 115;

Best Local Similarity 93.4%; Pred. No. 1.29e-34;

Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 24 ltqspatlsppgeratlscrasqsvsyawyyqkpgqprlliydasnratgiparfs 83

QY 3 LTQSPATLSLSPGERATLSQSPASQSVNKYLAWYQKPGQAPPLLIYDASNRTATGIPARFS 62

Db 84 gsgsgtdftltisslepedfavyycqrsnw 114

QY 63 GSGSGTDFLTISNLEPEDFAVYCYQQRSDW 93

RESULT 10

ID W03947 standard; Protein; 115 AA.

AC W03947;

DT 14-APR-1997 (first entry)

DE DNA fragment vk65.5, variable kappa chain protein product.

KW Variable; kappa chain; gene segment; human; DNA fragment; vk65.5;

KW unrearranged; light chain; minilocus; transgene; transgenic; mouse;

KW production; heterologous; antibody; gamma; immunoglobulin.

OS Homo sapiens.

PN US5545806-A.

PD 13-AUG-1996.

PF 29-AUG-1990; 574748.

PR 29-AUG-1990; US-574748.

PR 31-AUG-1990; US-575962.

PR 17-DEC-1991; US-810279.

PR 18-MAR-1992; US-853408.

PR 23-JUN-1992; US-904068.

PR 16-DEC-1992; US-900860.

PA (GENP-) GENPHARM INT INC.

PI Kay RM, Lonberg N;

DR *WPI: 96-383736/38.
 DR N-PSDB: T37181.
 PT Prodn. of heterologous human immunoglobulin(s) - by immunising
 PT transgenic mice
 PS Example 21; Fig 42; 94pp; English.
 CC The present sequence is the protein product of the variable kappa
 CC chain gene segment containing human DNA fragment, vk65.5, which
 CC was co-injected along with the human DNA fragments vk65.3, vk65.8
 CC and vk65.15 into half day mouse embryo pronuclei, to generate an
 CC unrearranged light chain minilocus transgene. The resulting
 CC transgenic mice can be used for the production of heterologous
 CC (i.e. human) antibodies against specific antigens, this comprises
 CC immunising a mouse with a preselected antigen and collecting
 CC antigen binding heterologous human gamma immunoglobulins.
 SQ Sequence 115 AA;
 Query Match 84.0%; Score 620; DB 20; Length 115;
 Best Local Similarity 93.4%; Pred. No. 1.29e-34;
 Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Db 24 ltqspatlslegratlsrscasqgvsylyawvqkpgqaprllydasnratgiparfs 83
 QY 3 ltqspatlslegratlsrscasqgvsylyawvqkpgqaprllydasnratgiparfs 62
 Db 84 gsgqtdftltisrlepedfavyvccqrsnw 114
 QY 63 GSGSGTDFTLTISNLEPEDFAVYVCQQRSDW 93
 RESULT 11
 ID R54275 standard; protein: 109 AA
 AC R54275;
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 41 19.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
 KW neutralisation; monoclonal antibody; light chain; variable region;
 KW framework region; complementarity determining region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57
 FT /label= CDR2
 FT Region 58..89
 FT /label= FR3
 FT Region 90..97
 FT /label= CDR3
 FT Region 98..109
 FT /label= FR4
 PN WO9407922-A.
 PD 14-APR-1994.
 PF 30-SEP-1993; U093328.
 PR 30-SEP-1992; US-954148.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Claim 11; Page 215-216; 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC diclontic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VL region sequence R54275 neutralises HIV1
 CC gp41.

SQ Sequence 109 AA;
 Query Match 83.5%; Score 616; DB 19; Length 109;
 Best Local Similarity 84.9%; Pred. No. 2.48e-34;
 Matches 90; Conservative 5; Mismatches 10; Indels 1; Gaps 1;
 Db 2 aeltqspatlslegratlsrscasqgvsylyawvqkpgqaprllydasnratgipd 61
 QY 1 aeltqspatlslegratlsrscasqgvsylyawvqkpgqaprllydasnratgipa 59
 Db 62 rfsgsgtdftltisrlepedfavyvccqgsgstfgggtkveik 107
 QY 60 RFSGSGTDFTLTISNLEPEDFAVYVCQQRSDWVTFGGGKVEIK 105
 RESULT 12
 ID W01320 standard; Protein, 109 AA.
 AC W01320;
 DT 29-JAN-1997 (first entry)
 DE VL of Fab, DL 41 19, binds to HIV gp41.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB; HIV, human immunodeficiency virus; glycoprotein, gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1 23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57
 FT /label= CDR2
 FT Region 58..89
 FT /label= FR3
 FT Region 90..97
 FT /label= CDR3
 FT Region 98..109
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example 3; Fig 19; 366pp; English.
 CC The sequences given in W01320-24 represent the light chain variable
 CC regions (VH) of a series of antibody fragments (FAB's) which are
 CC immunoreactive with HIV glycoprotein gp41. This sequence represents
 CC the sequence of the clone, DL 41 19. These sequences represent light
 CC chains which bind to the heavy light chain clones given in W01315-19. A
 CC monoclonal antibody containing one of these Fab sequences may have the
 CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity
 CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.
 CC The MAB may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 109 AA;
 Query Match 83.5%; Score 616; DB 19; Length 109;
 Best Local Similarity 84.9%; Pred. No. 2.48e-34;
 Matches 90; Conservative 5; Mismatches 10; Indels 1; Gaps 1;
 Db 2 aeltqspatlslegratlsrscasqgvsylyawvqkpgqaprllydasnratgipd 61
 QY 1 aeltqspatlslegratlsrscasqgvsylyawvqkpgqaprllydasnratgipa 59
 Db 62 rfsgsgtdftltisrlepedfavyvccqgsgstfgggtkveik 107
 QY 60 RFSGSGTDFTLTISNLEPEDFAVYVCQQRSDWVTFGGGKVEIK 105

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RESULT 13
ID R56286 standard; Protein: 109 AA.
AC R56286;
DT 04-MAR-1995 (first entry)
DE Light chain of Amb al-specific IgG4 antibody.
KW Allergen-specific immunoglobulin A; IgA; AL 15-5.2; light chain;
KW Allergen Amb a 1; ragweed; Ambrosia elator.
OS Synthetic.
PN W09414475-A.
PD 07-JUL-1994.
PF 20-DEC-1993; U12501.
PR 21-DEC-1992; US-994126.
PA (TANO-) TANOX BIOSYSTEMS INC.
PI Chang TW;
DR WPI: 94-234353/28.
DR N-PSDB; Q66538.
PT Compsn. contg. allergen specific IgA for treating mucosal tissue
PT - and conjugates of allergen specific Ig with polymer, for
PT treating IgE mediated allergies and for isolation of specific
PT allergens
PS Example; Page 27-28; 36pp; English.
CC Blood samples were collected from patients immunised with allergens
CC including ragweed (Ambrosia elator) extracts. The dominant allergen
CC in short ragweed is Amb a 1. Purified PBIs were immortalised and
CC then fused with mouse myeloma cell line 653 and the resultant clones
CC were screened using Amb a 1 protein. A single cell subclone AL 16-5.2,
CC secreting Amb al-specific IgG4, kappa antibody was selected. Total
CC RNA was prep'd. from the AL 16-5.2 cells and first strand cDNA was
CC pred. using oligo dt primers. When the first strand cDNA was used as
CC the template, and the 5' and 3' kappa light chain primers (Q66540,
CC Q66541) were used in PCR and amplified band of the expected size was
CC noted. The DNA sequence of several subclones contg. this amplified
CC DNA fragment was determined. The sequence and its deduced AA
CC sequence are shown in Q66538 and R56286. Comparison of the deduced
CC AL 16-5.2 L-chain sequence with human V region sequences indicates
CC that it is a member of the human VK III subgp.
SQ Sequence 109 AA;

Query Match 82.8%; Score 611; DB 10; Length 109;
Best Local Similarity 82.1%; Pred No. 5 61e-34;
Matches 87; Conservative 10; Mismatches 5; Indels 4; Gaps 4,

Db 4 ltqspgtlslspgeratiscrasqsvsnlyawqkpgqaprllyvgastatdipd 63
QY 3 LTQSPATLSLSPGEPATLSCRASQSVN-KYLAWYQQKPKGAPRLIYDASNRAIGIPARF 61

Db 64 tsgsgtdftltisrlepdefavyyccqfnsqw-tfgggtkveik 108
QY 62 SGSGSGTDFTLTISNLEPDEFVAVYCCQ-R-SDWVTFGGGTKEIK 105

RESULT 14
ID W01322 standard; Protein: 111 AA.
AC W01322;
DT 29-JAN-1997 (first entry)
DE VL of Fab, GL 41 1, binds to HIV gp41.
KW Heavy chain, light chain, variable region, VH, monoclonal antibody,
KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1 23
FT /label= FR1
FT Region 24...35
FT /label= CDR1
FT /label= FR2
FT /label= FR2
FT /label= CDR2
FT /label= FR3
FT /label= FR3
FT /label= CDR3
FT /label= FR4
FN W09407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCRI ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/16.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo

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PT or in vitro diagnosis and for passive immuno-therapy
PS Claim 11; Para 217; 248pp: English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAb regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VL region sequence R54277 neutralises HIV1
CC gp41.
SQ Sequence 111 AA;

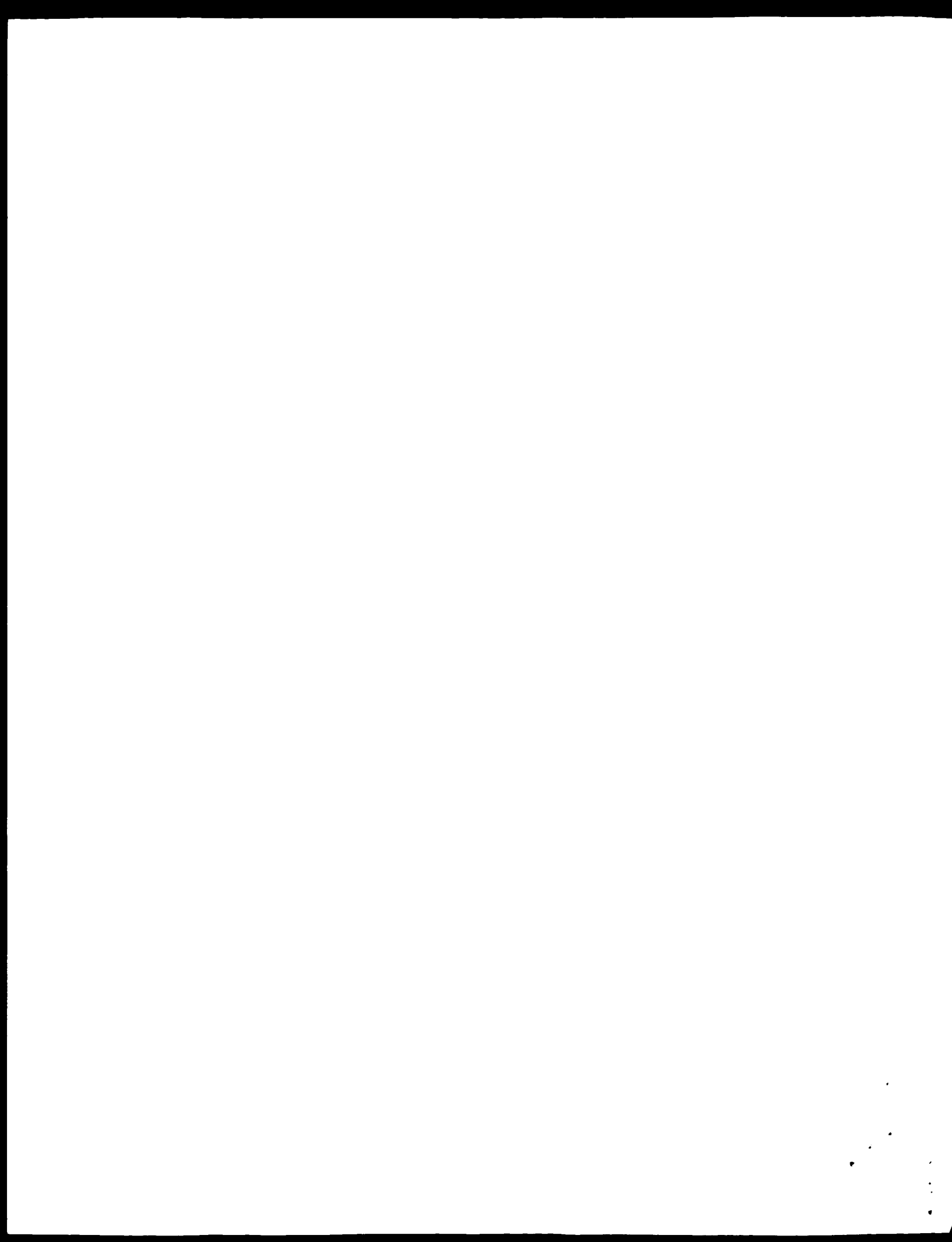
Query Match      82.4%: Score 608; DB 10; Length 111;
Best Local Similarity 83.0%: Pred. No. 9,15e-34;
Matches 88; Conservative 7; Mismatches 10; Indels 1; Caps 1;

Ddb 2 aeltqspqtislspgeratiscragsvngylwygkpkgaqrlllygastratidp 61
QOY 1 AELTQSPTATLSLSPGERATISCPASGSVVK-VLAWYQQKPKGAPRLIYYASNPA75IPA 59

Ddb 62 rfsugsgdaaftlairslepdedfavyvycqqyagshftfaqqtkleik 107
QOY 60 RFSUGSGDTFTLTITSLNLEPEFAFVVCQQPQSDWTFGGGTGVKVIK 105

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Search completed: Tue Feb 24 07:20:37 1998
Job time : 30 secs.




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RESULT 2
ID KV3L_HUMAN STANDARD: PRT: 129 AA.
AC P18135;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAI).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: P18022; K3HUHA.
DE HSSP: P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HAI).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 14073 MW: 2044885E CRC32:

Query Match 92.0%; Score 701; DB 5; Length 129;
Best Local Similarity 94.3%; Pred. No. 2.79e-133;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 24 ltspggtlslspgeratlscrasqsvssylawyyqkqpgqaprllygassratgipdrf 83
QY 3 LTQSPGTLSPGERATLSGCRASQSVSSNYLAWYQQRPGQAPRLLYGASSRATGIPDRF 62
|||||
Db 84 sgsqsgtdftltisrlepedfavyycqygsprtfqgqkveik 128
QY 63 SSGSGTGDTFTLTISRLPEDFAVYYCQLYGNRSRWTFGQGTKEIK 107
|||||

RESULT 3
ID KV3B_HUMAN STANDARD: PRT: 109 AA.
AC P01620;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (SIE).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPPA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01892; K3HUSI.
DE HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11775 MW: 6085005D CRC32:

Query Match 89.9%; Score 685; DB 5; Length 109;

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Best Local Similarity 91.4%; Pred. No. 1.55e-129;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltspggtlslspgeratlscrasqsvssylawyyqkqpgqaprllygassratgipdrf 63
QY 3 LTQSPGTLSPGERATLSGCRASQSVSSNYLAWYQQRPGQAPRLLYGASSRATGIPDRF 62
|||||
Db 64 sgsqsgtdftltisrlepedfavyycqygsprtfqgqkveik 108
QY 63 SSGSGTGDTFTLTISRLPEDFAVYYCQLYGNRSRWTFGQGTKEIK 107
|||||

RESULT 4
ID KV3E_HUMAN STANDARD: PRT: 109 AA.
AC P01623;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (WOL).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046598.
RA ANDREWS D.W., CAPPA J.D.;
RL BIOCHEMISTRY 20:5816-5822(1981).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A01896; K3HUMI.
DE HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11746 MW: 7D8F5D75 CRC32:

Query Match 89.9%; Score 685; DB 5; Length 109;
Best Local Similarity 92.4%; Pred. No. 1.55e-129;
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltspggtlslspgeratlscrasqsvssylawyyqkqpgqaprllygassratgipdrf 63
QY 3 LTQSPGTLSPGERATLSGCRASQSVSSNYLAWYQQRPGQAPRLLYGASSRATGIPDRF 62
|||||
Db 64 sgsqsgtdftltisrlepedfavyycqygsprtfqgqkveik 108
QY 63 SSGSGTGDTFTLTISRLPEDFAVYYCQLYGNRSRWTFGQGTKEIK 107
|||||

RESULT 5
ID KV3D_HUMAN STANDARD: PRT: 109 AA.
AC P01622;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (TI).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 72188439.
RA SUTER L., RARNIKOL H.U., WATANABE S., HILSCHMANN N.;
PL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:189-208(1972).
CC -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MAPKPEP.
CC ACTIVITY.
DR PIR: A01895; K3HUTI.
DE HSSP: P01607; 2IMM.
KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11789 MW: D03795B1 CRC32:

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Query Match      88.5%;      Score 674;   DB 5;   Length 109;
Best Local Similarity 90.5%;   Pred. No. 5,760-127;
Matches 95; Conservative 6; Mismatches 4; Indels

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Db 4 !tspgtlslspgeratlscrascsvnsflawyqkpgdaprlllyvassratgipdrf 63

0Y
3 LTOSPCTSLTSPERATUTTAZVSNYLAWCHHAGIAPALLIVASPAISPIRE 62

Db 64 sqsqsqtdftltisrlepedfavvycqyqsspsstfqgatkvelk 108

04 63 SGSGSGTDETLTISRLEPEDFAVYVYCOLYGNSPWTEGOGTKVEIK 107

RESULT	6	STANDARD	PRT
ID	KV3A_HUMAN		108 AA
AC	P01619		
AD	21-JUL-1986	(REL. 01, CREATED)	
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)	
DT	20-MAR-1987	(REL. 04, LAST ANNOTATION UPDATE)	
DE	IG KAPPA CHAIN V-III REGION (B6)		

OC HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VEPTERRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: PRIMATES.
 [1]
 RP SEQUENCE.
 RA MILSTEIN C.;
 RL FERS LETT. 2:301-304(1969).
 CC -!- THIS IS A RENCE-JONES PROTEIN
 PIR: A01891; K3H06.
 KW HSSP: P01607; IMCP.
 DR IMMUNOGLOBULIN V REGION: RENCE-JONES PROTEIN.
 FT DISULFID 23 84
 FT NON_TER 108 108
 FT SEQUENCE 108 AA: 11635 MW 4606666 GRC12:

Query Match 88.18; Score 671; DB 5; Length 1

Best Local Similarity	84.88%	Pred No	2,896-126;
Matches	89;	Conservative	12;
		Mismatches	4;
		Index	

4	ltzspgtislsgqraalscraslslnylawyqkqkqcaprllmyqvssratdip	
Db		
3	ltfsspttltslspgpatlscpqssvsnv:AWQPPFCAPPELLVGCSSPATC:P	
QY		
64	sgsgsgadtltslrzlpdzfavyccqgyassftfgqskleik 108	
Db		
63	sgsgsgdtftltlspfprrfavycolyngswtfcggtkvik 107	
QY		

Q	RESULT	7	STANDARD:	PRT:	109 AA
1	Q	Q	Q	Q	Q
2	Q	Q	Q	Q	Q
3	Q	Q	Q	Q	Q
4	Q	Q	Q	Q	Q
5	Q	Q	Q	Q	Q
6	Q	Q	Q	Q	Q
7	Q	Q	Q	Q	Q
8	Q	Q	Q	Q	Q
9	Q	Q	Q	Q	Q
10	Q	Q	Q	Q	Q
11	Q	Q	Q	Q	Q
12	Q	Q	Q	Q	Q
13	Q	Q	Q	Q	Q
14	Q	Q	Q	Q	Q
15	Q	Q	Q	Q	Q
16	Q	Q	Q	Q	Q
17	Q	Q	Q	Q	Q
18	Q	Q	Q	Q	Q
19	Q	Q	Q	Q	Q
20	Q	Q	Q	Q	Q
21	Q	Q	Q	Q	Q
22	Q	Q	Q	Q	Q
23	Q	Q	Q	Q	Q
24	Q	Q	Q	Q	Q
25	Q	Q	Q	Q	Q
26	Q	Q	Q	Q	Q
27	Q	Q	Q	Q	Q
28	Q	Q	Q	Q	Q
29	Q	Q	Q	Q	Q
30	Q	Q	Q	Q	Q
31	Q	Q	Q	Q	Q
32	Q	Q	Q	Q	Q
33	Q	Q	Q	Q	Q
34	Q	Q	Q	Q	Q
35	Q	Q	Q	Q	Q
36	Q	Q	Q	Q	Q
37	Q	Q	Q	Q	Q
38	Q	Q	Q	Q	Q
39	Q	Q	Q	Q	Q
40	Q	Q	Q	Q	Q
41	Q	Q	Q	Q	Q
42	Q	Q	Q	Q	Q
43	Q	Q	Q	Q	Q
44	Q	Q	Q	Q	Q
45	Q	Q	Q	Q	Q
46	Q	Q	Q	Q	Q
47	Q	Q	Q	Q	Q
48	Q	Q	Q	Q	Q
49	Q	Q	Q	Q	Q
50	Q	Q	Q	Q	Q
51	Q	Q	Q	Q	Q
52	Q	Q	Q	Q	Q
53	Q	Q	Q	Q	Q
54	Q	Q	Q	Q	Q
55	Q	Q	Q	Q	Q
56	Q	Q	Q	Q	Q
57	Q	Q	Q	Q	Q
58	Q	Q	Q	Q	Q
59	Q	Q	Q	Q	Q
60	Q	Q	Q	Q	Q
61	Q	Q	Q	Q	Q
62	Q	Q	Q	Q	Q
63	Q	Q	Q	Q	Q
64	Q	Q	Q	Q	Q
65	Q	Q	Q	Q	Q
66	Q	Q	Q	Q	Q
67	Q	Q	Q	Q	Q
68	Q	Q	Q	Q	Q
69	Q	Q	Q	Q	Q
70	Q	Q	Q	Q	Q
71	Q	Q	Q	Q	Q
72	Q	Q	Q	Q	Q
73	Q	Q	Q	Q	Q
74	Q	Q	Q	Q	Q
75	Q	Q	Q	Q	Q
76	Q	Q	Q	Q	Q
77	Q	Q	Q	Q	Q
78	Q	Q	Q	Q	Q
79	Q	Q	Q	Q	Q
80	Q	Q	Q	Q	Q
81	Q	Q	Q	Q</	

[illegible]

RESULT 8
ID KV3H HUMAN
STANDARD: DPT: 129 AA.

AC 504267; (P)
DT 20-MAR-1987 (REL. 04, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-II REGION (CII) (RHUMATOID FACTOR).
DS HOMO SAPIENS (HUMAN).
CS EUKARYOTA; METAZOA;
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUKARYOTA; PRIMATES.

AN	(1)	SEQUENCE FROM N A.	
RP		MEDLINE: 86177570.	
RA		JIRIK F.P., SORGE J., PONG S., HEITMANN J.G., GUO J.G., CHEN P.P.	
RX		GOLDFIEN R., CARSON D.A.,	
PL		PROC. NATL. ACAD. SCI. U.S.A. 83:2195-2196(1986).	
PA		EMBL: M12740; G553486; -	
DR		PIF: A01898; K3HTCL	
DP		HSSP: P01607; 1AAG.	
KW		IMMUNOGLOBULIN V REGION; SIGNAL.	
FT		SIGNAL	1 20
FT		CHAIN	21 129
FT		DOMAIN	21 43
FT		DOMAIN	44 54
FT		COMPLEMENTARITY-DETERMINING 1.	

FT	DOMAIN	70	76	COMPLEMENTARITY-DETERMINI
FT	DOMAIN	70	76	COMPLEMENTARITY-DETERMINI

FT	DOMAIN	77	108	FRAMEWORK 3
FT	DOMAIN	109	118	COMPLEMENTARITY-DETERMINI

[illegible]

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DR HSSP: P01607: 1AAG.
KW IMMUNOGLOBULIN V REGION: SIGNAL: HYBRIDOMA.
FT NON_TER 1 1 4
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION (NGS).
FT DISULFID 27 93 BY SIMILARITY.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 99A75223 CRC32;

Query Match 81.6%; Score 622; DB 5; Length 100;
Best Local Similarity 93.5%; Pred. No. 7.55e-115;
Matches 87; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 8 ltqspgtlslspgeratlscrasqsvssylawyqkqgqprlllygatsratgipdrf 67
QY 3 LTQSPGTLSLSPGERATLSCPASQSVSSNYLAWYQPPQAPPLLIYGASSRATGIPDPF 62

Db 68 sgsasgtdftltisrlepedfavyccqyansq 100
QY 63 SGSGSGTDTLTISRLEPEDFAVYCCYQYNSR 95

RESULT 10
ID KV3K_HUMAN STANDARD: PPT: 128 AA
AC P06311;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96041852.
RA KLOBECK H.G.; MEINDL A.; COMERIATO G.; SOLOMON A.; ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
DR EMBL; Z00021; G33179; -.
DR PIR; A01899; K3HU41.
DR HSSP; P01607; 3HFH.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IARC/BL41).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 54 FRAMEWORK 2.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;

Query Match 80.2%; Score 611; DB 5; Length 128;
Best Local Similarity 85.7%; Pred. No. 2.71e-112;
Matches 90; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Db 24 ltqspgtlslspgeratlscrasqsvsn-lawyqkqgqprlllydassrangipdrf 82
QY 3 LTQSPGTLSLSPGERATLSCPASQSVSSNYLAWYQPPQAPPLLIYGASSRATGIPDPF 62

Db 83 sgsasgtdftltisrlepedfavyccqyansqpytqgqtkleik 127
QY 63 SGSGSGTDTLTISRLEPEDFAVYCCYQYNSRWTFQGTKEIK 107

RESULT 11
ID KV3F_HUMAN STANDARD: PPT: 109 AA.
AC P01624;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)

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DE IG KAPPA CHAIN V-III REGION (POM).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
PN [1]
RP SEQUENCE.
PA KIAPPER D.G.; CAPPA J.D.;
PL ANN. INST. PASTEUR IMMUNOL. 127C:261-271(1976)
CC -I- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
DR PIR; A01897; K3HUPM.
DR HSSP; P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; A0C42C88 CRC32;

Query Match 79.4%; Score 605; DB 5; Length 109;
Best Local Similarity 79.0%; Pred. No. 6.69e-111;
Matches 83; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Db 4 mtqspvtlsvpgeratlscrasqslsnylawyqkqgqprlllygatsratgiparf 63
QY 3 LTQSPGTLSLSPGERATLSCPASQSVSSNYLAWYQPPQAPPLLIYGASSRATGIPDPF 62

Db 64 sgsasgtdftltisrlepedfavyccqyansqprlllygatsratgiparf 108
QY 63 SGSGSGTDTLTISRLEPEDFAVYCCYQYNSRWTFQGTKEIK 107

RESULT 12
ID KV3I_HUMAN STANDARD: PPT: 115 AA.
AC P04433;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85087932.
PA PECH M.; ZACHAU H.G.;
PL NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR EMBL; X01668; ; NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR HSSP; P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION (VG).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 37E182FC CRC32;

Query Match 73.5%; Score 560; DB 5; Length 115;
Best Local Similarity 72.0%; Pred. No. 1.72e-100;
Matches 80; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Db 24 ltqspgtlslspgeratlscrasqsvssylawyqkqgqprlllydassrangiparf 82
QY 3 LTQSPGTLSLSPGERATLSCPASQSVSSNYLAWYQPPQAPPLLIYGASSRATGIPDPF 62

Db 83 sgsasgtdftltisrlepedfavyccq 109
QY 63 SGSGSGTDTLTISRLEPEDFAVYCCQ 89

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RESULT 13
ID KV3J_HUMAN STANDARD: PRT: 116 AA.
AC P04434:
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DE 01-NOV-1986 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (VH) (FRAGMENT)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85087932
RA PECH M., ZACHAU H.G.
PC NUCLEIC ACIDS RES 12:9229-9236(1984)
DR EMRL: X02725; -- NOT ANNOTATED.
DR PIR: A01901; K3HUVH.
DR HSSP: P01607; IMCP.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION (VH)
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1
FT DOMAIN 44 55 FRAMEWORK 2
FT DOMAIN 56 70 FRAMEWORK 3
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 78 109 FRAMEWORK 3
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116
SQ SEQUENCE 116 AA: 12757 MW: 27FA1BCE CPO32:

Query Match 73.2% Score 558; DB 5; Length 116;
Best Local Similarity 87.4% Pred. No. 4 99e-100;
Matches 76; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db 24 mtgsptslspgervlscrasqssvssyltwyqkpgqgprlllygastatrsiparf 83
QY 3 LTQSPGTLSPGERATLSCRASQSSVSSNYLAWYQPPGQAPPELLYGGASSPATGIPDR 62
Db 84 sqsgsgtdftltisslqpedfavyvqc 110
QY 63 SGSGSGTDFTLISRLPEDFAVYVQC 89

RESULT 14
ID KVM_HUMAN STANDARD: PRT: 108 AA
AC P01605:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (LAV).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 7703198
RA CAPRA J.D., KLAPPER D.G.
HL SCAND. J. IMMUNOL. 5:675-684(1976).
CC -1- THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN PM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
DR PIR: A01871; K1HUYL.
DR HSSP: P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
SQ SEQUENCE 108 AA: BRADA251 CPO32:

Query Match 60.1% Score 529; DB 5; Length 108;
Best Local Similarity 53.2% Pred. No. 4 01e-93;
Matches 67; Conservative 23; Mismatches 15; Indels 1; Gaps 1;

Db 3 qmtqpsissasvqdrvtltorasqdrindltwyqkpgqgprlllygastatrsiparf 61
QY 2 ELTQSPGTLSPGERATLSCRASQSSVSSNYLAWYQPPGQAPPELLYGGASSPATGIPDR 61
Db 62 fsgsgsgtdftltisslqpedfavyvqc 107
QY 62 FSQSGSGTDFTLISRLPEDFAVYVQYGLYGNSPWTFQSGTKVEIK 107

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Search completed: Tue Feb 24 07:17:24 1998
Job time : 14 secs.

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FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
SQ SEQUENCE 108 AA: 2222RPOC CPO32:

Query Match 70.5% Score 537; DB 5; Length 108;
Best Local Similarity 67.0% Pred. No. 3 42e-95;
Matches 71; Conservative 21; Mismatches 13; Indels 1; Gaps 1;

Db 3 qmtqpsissasvqdrvtltorasqdrindltwyqkpgqgprlllygastatrsiparf 61
QY 2 ELTQSPGTLSPGERATLSCRASQSSVSSNYLAWYQPPGQAPPELLYGGASSPATGIPDR 61
Db 62 fsgsgsgtdftltisslqpedfavyvqc 107
QY 62 FSQSGSGTDFTLISRLPEDFAVYVQYGLYGNSPWTFQSGTKVEIK 107

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RESULT 15
ID KVM_HUMAN STANDARD: PRT: 108 AA.
AC P01610:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-I REGION (WEA).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 83273707.
RA GONI F., FRANGIONE B.;
PL PROC. NATL. ACAD. SCI. U.S.A. 80:4837-4841(1983).
CC -1- THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRIDYLATE GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR: A01876; K1HWE.
DR HSSP: P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION: MONOCLONAL ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
SQ SEQUENCE 108 AA: BRADA251 CPO32:

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Query Match 60.1% Score 529; DB 5; Length 108;
Best Local Similarity 53.2% Pred. No. 4 01e-93;
Matches 67; Conservative 23; Mismatches 15; Indels 1; Gaps 1;

Db 3 qmtqpsissasvqdrvtltorasqdrindltwyqkpgqgprlllygastatrsiparf 61
QY 2 ELTQSPGTLSPGERATLSCRASQSSVSSNYLAWYQPPGQAPPELLYGGASSPATGIPDR 61
Db 62 fsgsgsgtdftltisslqpedfavyvqc 107
QY 62 FSQSGSGTDFTLISRLPEDFAVYVQYGLYGNSPWTFQSGTKVEIK 107

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 W P R E F H
 (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Feb 24 07:17:42 1998; MasPar time 7.33 Seconds
 Tabular output not generated 444.542 Million cell updates/sec

Title: >US-08-844-215-8
 Description: (1-107); from US08844215 pep
 Perfect Score: 762
 Sequence: 1 AFLTQSPGTLSTSPGFRATL

Scoring table: PAM 150
 Gap 11
 Searched: 95051 seqs, 30459580 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r53
 1:unann1 2:unann2 3:unann3 4:unann4 5:unann5 6:unann6 7:unann7
 8:unann8 9:unann9 10:unann10 11:unann11 12:unann12 13:unann13
 14:unann14 15:unann15 16:unann16 17:unann17 18:unann18

Statistics: Mean 40.550; Variance 149.293; scale 0.272
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	712	93.4	108	7	Ig kappa chain V-III	2 17e-63
2	712	93.4	129	2	K3HUHI	2 17e-63
3	710	93.2	107	7	Ig kappa chain V-III	3 63e-63
4	702	92.1	109	7	Ig kappa chain V-III	2 85e-63
5	701	92.0	129	2	K3HUHI	3 68e-63
6	700	91.9	109	7	Ig kappa chain V-III	4 76e-63
7	697	91.5	128	7	Ig kappa chain V-III	1 03e-61
8	695	91.2	109	7	Ig kappa chain V-III	1 72e-61
9	694	91.1	109	7	Ig kappa chain V-III	2 23e-61
10	692	90.8	109	7	Ig kappa chain V-III	3 73e-61
11	692	90.8	109	7	Ig kappa chain V-III	3 73e-61
12	691	90.7	109	7	Ig kappa chain V-III	4 82e-61
13	689	90.4	110	7	Ig kappa chain V-III	8 07e-61
14	688	90.3	109	7	Ig kappa chain V-III	1 04e-60
15	687	90.2	109	7	Ig kappa chain V-III	1 15e-60
16	686	90.0	129	7	Ig kappa chain V-III	1 74e-60
17	685	89.9	109	7	Ig kappa chain V-III	1 74e-60
18	685	89.9	109	7	Ig kappa chain V-III	2 26e-60
19	685	89.9	109	7	Ig kappa chain V-III	2 26e-60
20	684	89.9	109	7	Ig kappa chain V-III	2 92e-60

21	683	89.6	110	7	E30607	Ig kappa chain V-III	3 77e-60
22	681	89.4	109	7	G30507	Ig kappa chain V-III	6 31e-60
23	681	89.4	114	7	S46375	Ig kappa chain V-III	6 31e-60
24	677	88.8	109	7	F30601	Ig kappa chain V-III	1 76e-59
25	676	88.7	122	7	S46572	anti-Sm antibody V1	2 26e-59
26	674	88.5	109	2	K3HUHI	Ig kappa chain V-III	3 81e-59
27	673	88.3	108	7	B30608	Ig kappa chain V-III	4 93e-59
28	671	88.1	138	2	K3HUHI	Ig kappa chain V-III	9 23e-59
29	670	87.9	108	7	E30609	Ig kappa chain V-III	1 06e-58
30	666	87.4	130	7	S20637	Ig kappa chain V-III	2 97e-58
31	664	87.1	129	7	S40125	Ig kappa chain - hum	4 96e-58
32	662	86.9	110	7	S4120	Ig kappa chain V-III	8 29e-58
33	662	86.9	124	7	S20633	Ig kappa chain - hum	8 29e-58
34	661	86.7	109	7	S47181	Ig kappa chain - hum	1 07e-57
35	660	86.5	129	7	A32274	Ig kappa chain - hum	1 39e-57
36	658	86.4	109	2	K3HUHI	Ig kappa chain V-III	2 31e-57
37	656	86.1	121	7	S40327	Ig kappa chain - hum	3 87e-57
38	655	86.0	104	7	PH0564	Ig kappa chain V-III	5 00e-57
39	646	84.8	111	7	S23628	Ig kappa chain V-III	5 02e-56
40	638	83.7	127	7	S40380	Ig kappa chain V-III	3 89e-55
41	631	82.8	130	7	S40360	Ig kappa chain - hum	2 30e-54
42	630	82.7	145	7	S20631	Ig kappa chain - hum	3 02e-54
43	629	82.5	108	7	S33988	Ig kappa chain V-III	3 89e-54
44	629	82.5	128	7	S40379	Ig kappa chain V-III	3 89e-54
45	627	82.3	128	7	A56701	Ig kappa chain V-III	6 49e-54

ALIGNMENTS

RESULT 1
 ENTRY C30608 #type fragment
 TITLE Ig kappa chain V-III region (Pie) - human (fragment)
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
 ACCESSIONS C30608
 REFERENCE A30601
 #authors Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjunilla, M.L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.
 #journal J. Immunol. (1989) 142:3158-3163
 #title Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.
 #accession C30608
 #status preliminary
 #molecule_type protein
 #residues 1-108 #label GON
 CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
 KEYWORDS heterotetramer: immunoglobulin
 SUMMARY #length 108 #checksum 1607

Query Match 93.4% Score 712. PR 7. Length 108:
 Best Local Similarity 94.3% Freq. No. 2.17e-63
 Matches 99, Conservative 4, Mismatches 2, Indels 0, Gaps 0:
 Db 4 LTPSPGTLSTSPGFRATLSCASVSNNYLAWSYVQKPKQAPRIIYQSSSTATQIDRT 53
 QY 3 LTPSPGTLSTSPGFRATLSCASVSNNYLAWSYVQKPKQAPRIIYQSSSTATQIDRT 52
 Db 64 SSGSGTDFLTISPIEPESFAVYQYQYSSPWTFGGKVEIK 108
 QY 63 SSGSGTDFLTISPIEPESFAVYQYQYSSPWTFGGKVEIK 107
 RESULT 2
 ENTRY K3HUHI #type complete
 TITLE Ig kappa chain precursor V-III region (Hic) - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 30-Jun-1997
 ACCESSIONS F30601
 REFERENCE F30601

authors Kipps, T. J.; Tomhave, E.; Chen, P. P.; Carson, D.A.
journal J. Exp. Med. (1988) 167:840-852
title Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.
cross-references MUID:88171307
accession P00021
molecule_type mRNA
residues 1-129 ##label KIP
comment The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.
GENETICS
gene GDB:IGKV3
cross-references GDB:136266
complex
description An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
classification **superfamily** immunoglobulin V region; immunoglobulin homology
keywords autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
feature
1-20 #domain signal sequence #status predicted #label SIG
21-129 #product Ig kappa chain V-III region (Hic) #status predicted #label MAR
21-117 #region V segment
44-55 #region complementarity-determining 1\
71-77 #region complementarity-determining 2\
110-117 #region complementarity-determining 3\
118-129 #region J segment (JK1)\
43-109 #disulfide_bonds #status predicted
summary #length 129 #molecular_weight 14070 #checksum 8174
query match 93.4%; Score 712; DB 2; Length 129;
best local similarity 94.3%; Pred. No. 2.17e-63;
matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
db 24 ltsgptlslspgeratlsrscrasqvssylawyqkqpgqaprllygassratgipdrf 83
qy 3 LTQSPGTLSPGERATLSRCPASQSVSSNYLAWYQRPQAPRLIYGCASSPATGIPDRF 62
db 84 ssgsgtdftltisrlepdefavyyqgyspwtfgggtkveik 128
qy 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRWTFGGKTVEIK 107
result 3
entry PH0965 #type fragment
title Ig kappa chain V region (G6+ CLL-BRA) - human (fragment)
organism #formal_name Homo sapiens #common_name man
date 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
accessions PH0965
reference PH0952
authors Martin, T.; Duff, S.F.; Carson, D.A.; Kipps, T.J.
journal J. Exp. Med. (1992) 175:983-991
title Evidence for somatic selection of natural autoantibodies.
cross-references MUID:9220289C
accession PH0965
status nucleic acid sequence not shown
molecule_type DNA
residues 1-107 ##label MAR
classification **superfamily** immunoglobulin V region; immunoglobulin homology
keywords heterotetramer; immunoglobulin
feature
1-21 #region framework 1\
22-32 #region complementarity-determining 1\
33-48 #region framework 2\
49-54 #region complementarity-determining 2\
55-87 #region framework 3\

88-95 #region complementarity-determining 3
summary #length 107 #checksum 7830
query match 93.2%; Score 710; DB 7; Length 107;
best local similarity 95.2%; Pred. No. 3.63e-63;
matches 100; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
db 2 ltsgptlslspgeratlsrscrasqvssylawyqkqpgqaprllygassratgipdrf 61
qy 3 LTQSPGTLSPGERATLSRCPASQSVSSNYLAWYQRPQAPRLIYGCASSPATGIPDRF 62
db 62 ssgsgtdftltisrlepdefavyyqgyspwtfgggtkveik 106
qy 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRWTFGGKTVEIK 107
result 4
entry D30601 #type fragment
title Ig kappa chain V-III region (Cur) - human (fragment)
organism #formal_name Homo sapiens #common_name man
date 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
accessions D30601
reference A30601
authors Goni, F. P.; Chen, P. P.; McGinnis, D.; Arjonilla, M. L.; Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.; Frangione, B.
journal J. Immunol. (1989) 142:3158-3163
title Structural and idiotypic characterization of the L chains of human IgM autoantibodies with different specificities.
cross-references MUID:89215279
accession D30601
status preliminary
molecule_type protein
residues 1-109 ##label GON
classification **superfamily** immunoglobulin V region; immunoglobulin homology
keywords heterotetramer; immunoglobulin
summary #length 109 #checksum 6151
query match 92.1%; Score 702; DB 7; Length 109;
best local similarity 94.3%; Pred. No. 2.85e-62;
matches 99; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
db 4 ltsgptlslspgeratlsrscrasqvssylawyqkqpgqaprllygassratgipdrf 63
qy 3 LTQSPGTLSPGERATLSRCPASQSVSSNYLAWYQRPQAPRLIYGCASSPATGIPDRF 62
db 64 ssgsgtdftltisrlepdefavyyqgyspwtfgggtkveik 108
qy 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRWTFGGKTVEIK 107
result 5
entry K3HUNA #type complete
title Ig kappa chain precursor V-III region (Hah) - human
organism #formal_name Homo sapiens #common_name man
date 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 30-May-1997
accessions P10022
reference P10021
authors Kipps, T.J.; Tomhave, E.; Chen, P.F.; Carson, D.A.
journal J. Exp. Med. (1988) 167:840-852
title Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.
cross-references MUID:88171307
accession P10022
molecule_type mRNA
residues 1-129 ##label KIP
comment The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.
GENETICS


```

ACCESSIONS H30601; E30601
REFERENCE A30601
#authors Gonl, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
          Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
          Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
#cross-references MUID:89215279
#accession H30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON1
#accession E30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON2
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5951

Query Match 91.1%; Score 694; DB 7; Length 109;
Best Local Similarity 93.3%; Pred. No. 2.23e-61;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltsgptlslspgeratlscrasqsvssylawygkqkqaprrlllygassratgipdrf 63
QY 3 LTOSPTLSLSPGERATLSQPASQSVSSNYLAWYQQRCPAPRLLIYGASSRATGIPDRF 62

Db 64 sgsgsgtdftltisrlepedfavyycqygsspytfgggtkveik 108
QY 63 SGSGSGTDFTLTISRLEPEDFAVYVCQLYGNSRWTFGGGTKEIK 107

RESULT 10
ENTRY F44151 #type fragment
TITLE Ig kappa chain V region (JM-01) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
16-Aug-1996
ACCESSIONS F44151
REFERENCE A44151
#authors Zebadee, S.L.; Barbas III, G.F.; Hwu, Y.L.; Caothien, R.H.;
          Graff, R.; DeGraw, J.; Pyati, J.; LaPolla, R.; Burton,
          D.P.; Lerner, R.A.; Thornton, G.B.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:3175-3179
#title Human combinatorial antibody libraries to hepatitis B surface
          antigen.
#accession F44151
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-109 #label ZEB
#note nucleotide translation not given
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5518

Query Match 90.8%; Score 692; DB 7; Length 109;
Best Local Similarity 91.6%; Pred. No. 3.73e-61;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 1 aeltspgtlslspgeratlscrasqsvfnylawygkqkqaprrlllygassratgipdr 60
QY 1 AELTSPGTLSLSPGERATLSQASQSVSSNYLAWYQQRCPAPRLLIYGASSRATGIPDR 60

Db 61 rfsgsgsgtdftltisrlepedfavyycqygsspytfgggtkveik 107
QY 61 RFSGSGSGTDFTLTISRLEPEDFAVYVCQLYGNSRWTFGGGTKEIK 107

RESULT 11
ENTRY F30607 #type fragment
TITLE Ig kappa chain V-III region (Bor) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man

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ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS F30607
REFERENCE A30601
#authors Gonl, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
          Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
          Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
#cross-references MUID:89215279
#accession F30607
#status preliminary
#molecule_type protein
#residues 1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 6514

Query Match 90.8%; Score 692; DB 7; Length 109;
Best Local Similarity 94.3%; Pred. No. 3.73e-61;
Matches 99; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 4 ltsgptlslspgeratlscrasqsvssylawygkqkqaprrlllygassratgipdrf 63
QY 3 LTOSPTLSLSPGERATLSQASQSVSSNYLAWYQQRCPAPRLLIYGASSRATGIPDRF 62

Db 64 sgsgsgtdftltisrlepedfavyycqygsspytfgggtkveik 108
QY 63 SGSGSGTDFTLTISRLEPEDFAVYVCQLYGNSRWTFGGGTKEIK 107

RESULT 12
ENTRY G30601 #type fragment
TITLE Ig kappa chain V-III region (Got) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
16-Aug-1996
ACCESSIONS G30601
REFERENCE A30601
#authors Gonl, F.P.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
          Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
          Frangione, B.
#journal J. Immunol. (1989) 142:3158-3163
#title Structural and idiotypic characterization of the L chains of
#cross-references MUID:89215279
#accession G30601
#status preliminary
#molecule_type protein
#residues 1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 109 #checksum 5641

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Best Local Similarity 92.4%; Pred. No. 4.82e-61;
Matches 97; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltsgptlslspgeratlscrasqsvssylawygkqkqaprrlllygassratgipdrf 63
QY 3 LTOSPTLSLSPGERATLSQASQSVSSNYLAWYQQRCPAPRLLIYGASSRATGIPDRF 62

Db 64 sgsgsgtdftltisrlepedfavyycqygsspytfgggtkveik 108
QY 63 SGSGSGTDFTLTISRLEPEDFAVYVCQLYGNSRWTFGGGTKEIK 107

RESULT 13
ENTRY S20635 #type complete
TITLE Ig kappa chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man

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DATE          20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
              16-Aug-1996
ACCESSIONS    S20635
REFERENCE      S20631
#authors      Lee, S. K.; Bridges, L. S.; Koopman, W. T.; Schroeder, H. W.
#submissions  submitted to the EMBL Data Library, April 1992
#accession    S20635
#status       preliminary
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#residues     1-110 #label LEE
#cross-references EMBL:Z11893
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 110 #molecular-weight 11965 #checksum 136

Query Match    90.4%; Score 689; DB 7; Length 110;
Best Local Similarity 91.4%; Pred. No. 8.07e-61;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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Qy 3 LTQSPGTLSPGGERATLSCPASQSVSSNVLAWYQQPQPGAPRLLYYGASSPATGIPDRF 62
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Db 66 sgsqsgtdftltisrlepedfavyycqyqdsprtfqggtkveik 110
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Qy 63 SGSGSGTDFTLTISRLEPEDFAVYVCQLYGNRWTFGQGTKEIK 107
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RESULT 14
ENTRY        PH0963 #type fragment
TITLE        Ig kappa chain V region (G6+ CLL-SM1) - human (fragment)
ORGANISM     #formal_name Homo sapiens #common_name man
DATE         17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
              16-Aug-1996
ACCESSIONS    PH0963
REFERENCE      PH0952
#authors      Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal      J. Exp. Med. (1992) 175:983-991
#title        Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession    PH0963
#status       nucleic acid sequence not shown
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KEYWORDS       heterotetramer; immunoglobulin
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35-50         #region framework 2\
51-56         #region complementarity-determining 2\
57-89         #region framework 3\
90-97         #region complementarity-determining 3
SUMMARY        #length 109 #checksum 5292

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Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Qy 3 LTQSPGTLSPGGERATLSCPASQSVSSNVLAWYQQPQPGAPRLLYYGASSPATGIPDRF 62
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Qy 63 SGSGSGTDFTLTISRLEPEDFAVYVCQLYGNRWTFGQGTKEIK 107
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RESULT 15
ENTRY        A30608 #type fragment
TITLE        Ig kappa chain V-III region (Son) - human (fragment)
ORGANISM     #formal_name Homo sapiens #common_name man
DATE         29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change

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              16-Aug-1996
ACCESSIONS    A30608
REFERENCE      A30601
#authors      Gotti, F.R.; Chen, F.P.; McGinnis, D.; Arjonilla, M.L.;
              Fernandez, J.; Carson, D.; Solomon, A.; Mender, E.;
              Frangione, B.
#journal      J. Immunol. (1989) 142:3158-3163
#title        Structural and idiotypic characterization of the L chains of
              human IgM autoantibodies with different specificities.
#cross-references MUID:89215279
#accession    A30608
#status       preliminary
#molecule_type protein
#residues     1-109 #label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
SUMMARY        #length 109 #checksum 6031

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Best Local Similarity 92.4%; Pred. No. 1.35e-60;
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Db 64 sgsqsgtdftltisrlepedfavyycqyqdsprtfqggtkveik 108
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Qy 63 SGSGSGTDFTLTISRLEPEDFAVYVCQLYGNRWTFGQGTKEIK 107
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Search completed: Tue Feb 24 07:18:03 1998
Job time : 21 secs.

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WATERMAN

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.
MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:44:44 1998; MasPar time 2.89 Seconds
Tabular output not generated. 188,570 Million cell updates/sec

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Description: (1-107) from US08844215.pep
Perfect Score: 762
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Scoring table: PAM 150
Gap 11
Searched: 56402 seqs, 5095871 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:PCR90 9:PCR91
10:PCR92 11:PCR93 12:PCR94 13:PCR95 14:PCR96
Statistics: Mean 27.478; Variance 143.457; scale 0.192

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
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2	697	91.5	108	7	US-08-276- Sequence 86, Applicati	1 95e-46
3	685	89.9	107	13	PCT-US95-0 Sequence 90, Applicati	1 80e-45
4	685	89.9	107	7	US-08-276- Sequence 90, Applicati	1 80e-45
5	685	89.9	108	6	US-08-477- Sequence 86, Applicati	1 80e-45
6	685	89.9	108	7	US-08-474- Sequence 86, Applicati	1 80e-45
7	685	89.9	108	5	US-07-634- Sequence 86, Applicati	1 80e-45
8	685	89.9	108	7	US-08-487- Sequence 86, Applicati	1 80e-45
9	684	89.8	108	13	PCT-US95-0 Sequence 99, Applicati	2 17e-45
10	684	89.8	108	7	US-08-276- Sequence 99, Applicati	2 17e-45
11	683	89.6	109	13	PCT-US93-0 Sequence 23, Applicati	2 61e-45
12	680	89.2	109	13	PCT-US95-0 Sequence 147, Applicati	4 55e-45
13	680	89.2	109	7	US-08-276- Sequence 147, Applicati	4 55e-45
14	670	87.9	104	13	PCT-US95-0 Sequence 100, Applicat	2 90e-44
15	670	87.9	104	7	US-08-276- Sequence 100, Applicat	2 90e-44
16	670	87.9	111	13	PCT-US95-0 Sequence 149, Applicat	2 90e-44
17	670	87.9	111	7	US-08-276- Sequence 149, Applicat	2 90e-44
18	662	86.9	108	7	US-08-276- Sequence 110, Applicat	1 28e-43
19	662	86.9	108	13	PCT-US95-0 Sequence 110, Applicat	1 28e-43
20	656	86.1	107	7	US-08-276- Sequence 87, Applicati	3 87e-43
21	656	86.1	107	13	PCT-US95-0 Sequence 87, Applicati	3 87e-43
22	641	84.1	108	13	PCT-US95-0 Sequence 95, Applicati	6 22e-42

23	641	84.1	108	7	US-08-276- Sequence 95, Applicati	6 22e-42
24	641	84.1	109	11	PCT-US93-0 Sequence 24, Applicati	6 22e-42
25	636	83.5	108	7	US-08-276- Sequence 88, Applicati	1 57e-41
26	636	83.5	108	13	PCT-US95-0 Sequence 88, Applicati	1 57e-41
27	628	82.4	107	13	PCT-US95-0 Sequence 118, Applicat	6 87e-41
28	628	82.4	107	7	US-08-276- Sequence 118, Applicat	6 87e-41
29	628	82.2	112	7	US-08-276- Sequence 151, Applicat	9 95e-41
30	626	82.2	112	13	PCT-US95-0 Sequence 151, Applicat	9 95e-41
31	625	82.0	116	7	US-08-053- Sequence 183, Applicat	1 20e-40
32	620	81.4	107	13	PCT-US95-0 Sequence 116, Applicat	3 01e-40
33	620	81.4	107	7	US-08-276- Sequence 116, Applicat	3 01e-40
34	618	81.1	104	13	PCT-US95-0 Sequence 92, Applicati	4 36e-40
35	618	81.1	104	7	US-08-276- Sequence 92, Applicati	4 36e-40
36	617	81.0	107	7	US-08-276- Sequence 117, Applicat	4 36e-40
37	617	81.0	107	13	PCT-US95-0 Sequence 117, Applicat	5 25e-40
38	615	80.7	105	7	US-08-276- Sequence 93, Applicati	7 59e-40
39	615	80.7	105	13	PCT-US95-0 Sequence 93, Applicati	7 59e-40
40	614	80.6	104	13	PCT-US95-0 Sequence 94, Applicati	9 13e-40
41	614	80.6	104	7	US-08-276- Sequence 94, Applicati	9 13e-40
42	602	79.0	107	13	PCT-US95-0 Sequence 120, Applicat	8 36e-39
43	602	79.0	107	7	US-08-276- Sequence 120, Applicat	8 36e-39
44	602	79.0	107	7	US-08-276- Sequence 115, Applicat	8 36e-39
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DT	01-JAN-1900					
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CC	APPLICANT:					
CC	TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES					
CC	TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS					
CC	NUMBER OF SEQUENCES: 170					
CC	COMPUTER PEADARIE FORM:					
CC	MEDIUM TYPE: Floppy disk					
CC	COMPUTER: IBM PC compatible					
CC	OPERATING SYSTEM: PC-DOS/MS-DOS					
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)					
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CC	FILING DATE: 11-JUL-1995					
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CC	APPLICATION NUMBER: US 08/276,852					
CC	FILING DATE: 18-JUL-1994					
CC	INFORMATION FOR SEQ ID NO: 86:					
CC	SEQUENCE CHARACTERISTICS:					
CC	LENGTH: 108 amino acids					
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	Best Local Similarity 92.5%, Pred No. 1 95e-46:					
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Db	61 FSGSGSGDTFTLTLSRLEPEDFAVYSCQOYCTSPWTFGQGTKEIK 106					
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DT    01-JAN-1900
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DE    Sequence 86, Application US/08276852.
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CC    Patent No. 5652138
CC    GENERAL INFORMATION:
CC    APPLICANT: Burton, Dennis R
CC    APPLICANT: Barbas, Carlos F
CC    APPLICANT: Lerner, Richard A
CC    TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC    TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC    NUMBER OF SEQUENCES: 170
CC    CORRESPONDENCE ADDRESS:
CC    ADDRESSEE: The Scripps Research Institute, Office of
CC    ADDRESSEE: Patent Counsel
CC    STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC    STREET: Mail Drop TPC8
CC    CITY: La Jolla
CC    STATE: CA
CC    COUNTRY: USA
CC    ZIP: 92037
CC    COMPUTER READABLE FORM:
CC    MEDIUM TYPE: Floppy disk
CC    OPERATING SYSTEM: PC-DOS/MS-DOS
CC    SOFTWARE: PatentIn Release #1.0, Version #1.25
CC    CURRENT APPLICATION DATA:
CC    APPLICATION NUMBER: US/08/276,852
CC    FILING DATE: 18-JUL-1994
CC    CLASSIFICATION: 514
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CC    APPLICATION NUMBER: US 08/178,302
CC    FILING DATE: 30-SEP-1993
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: US 07/954,148
CC    FILING DATE: 30-SEP-1992
CC    ATTORNEY/AGENT INFORMATION:
CC    NAME: Fitting, Thomas
CC    REGISTRATION NUMBER: 34,163
CC    REFERENCE/DOCKET NUMBER: SCP1452P
CC    TELECOMMUNICATION INFORMATION:
CC    TELEPHONE: 619-554-2937
CC    TELEFAX: 619-554-6312
CC    INFORMATION FOR SEQ ID NO: 86:
CC    SEQUENCE CHARACTERISTICS:
CC    LENGTH: 108 amino acids
CC    TYPE: amino acid
CC    TOPOLOGY: linear
CC    MOLECULE TYPE: protein
CC    SEQUENCE 108 AA; 11769 MW; 65957 CN;

Query Match      91.5%; Score 697; DB 7; Length 108;
Best Local Similarity 92.5%; Pred No 1 95e-46;
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGERATLSRQASQSVSNLYAWYQKPGQAPRLIYGVSNRATGIPDR 60
QY 2 ELTQSPGTLSPGERATLSRQASQSVSNLYAWYQKPGQAPRLIYGVSNRATGIPDR 61
Db 61 FSGSGSGDTFLTISRLEPEDFAVYCYQYGNVSVTFQGTKEIK 106
QY 62 FSGSGSGDTFLTISRLEPEDFAVYCYQYGNVSVTFQGTKEIK 107

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DT    01-JAN-1900
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CC    APPLICANT:
CC    TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC    TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC    NUMBER OF SEQUENCES: 170
CC    COMPUTER READABLE FORM:
CC    MEDIUM TYPE: Floppy disk
CC    OPERATING SYSTEM: PC-DOS/MS-DOS
CC    SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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CC    APPLICATION NUMBER: PCT/US95/08743
CC    FILING DATE: 11-JUL-1995
CC    PRIOR APPLICATION DATA:
CC    APPLICATION NUMBER: US 08/276,852
CC    FILING DATE: 18-JUL-1994
CC    INFORMATION FOR SEQ ID NO: 90:
CC    SEQUENCE CHARACTERISTICS:
CC    LENGTH: 107 amino acids
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CC    TOPOLOGY: linear
CC    MOLECULE TYPE: protein
CC    SEQUENCE 107 AA; 11705 MW; 62938 CN;

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Db 1 ELTQSPGTLSPGERATLSRQASQSVSNLYAWYQKPGQAPRLIYGVSNRATGIPDR 60
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DT    01-JAN-1900
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CC    Sequence 90, Application US/08276852
CC    Patent No. 5652138
CC    GENERAL INFORMATION:
CC    APPLICANT: Burton, Dennis R
CC    APPLICANT: Barbas, Carlos F
CC    APPLICANT: Lerner, Richard A
CC    TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC    TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC    NUMBER OF SEQUENCES: 170
CC    CORRESPONDENCE ADDRESS:
CC    ADDRESSEE: The Scripps Research Institute, Office of
CC    ADDRESSEE: Patent Counsel
CC    STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC    STREET: Mail Drop TPC8
CC    CITY: La Jolla
CC    STATE: CA
CC    COUNTRY: USA
CC    ZIP: 92037
CC    COMPUTER READABLE FORM:

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CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/276,852
 CC FILING DATE: 18-JUL-1994
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SCRI452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 90:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 107 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 107 AA: 11705 MW: 52938 CN:

Query Match 89.9%; Score 685; DB 7; Length 107;
 Best Local Similarity 89.6%; Pred. No. 1.80e-45;
 Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGERATLSCPASQSLNNYLAWYQKPGQAPLLYGSSTGTGIPDR 60
 QY 2 ELTQSPGTLSPGERATLSCPASQSVSSNYLAWYQKPGQAPLLYGSSTGTGIPDR 61
 Db 61 FSGSGSGDFTLTISRLEPEDFAVYQCYGNSVTFQGGTKLEIK 106
 QY 62 FSGSGSGDFTLTISRLEPEDFAVYQCYGNSRWFQGGTKVEIK 107

RESULT 5
 ID US-08-477-728-86 STANDARD: PRT: 108 AA.
 XX xxxxxx
 AC
 XX 01-JAN-1900
 DT
 DE Sequence 86, Application US/08477728.
 XX
 CC Sequence 86, Application US/08477728
 CC Patent No. 5585089
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend and Crew LLP
 CC STREET: Two Embarcadero Center, 8th Floor
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94111
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/477,728

CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002600
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 86:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 108 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 108 AA: 11590 MW: 64079 CN:

Query Match 89.9%; Score 685; DB 6; Length 108;
 Best Local Similarity 92.4%; Pred. No. 1.80e-45;
 Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 LTQSPGTLSPGERATLSCPASQSVSSNYLAWYQKPGQAPLLYGSSTGTGIPDR 63
 QY 3 LTQSPGTLSPGERATLSCPASQSVSSNYLAWYQKPGQAPLLYGSSTGTGIPDR 62
 Db 64 SSGSGSGDFTLTISRLEPEDFAVYQCYGNSLGHTRQGGTKVEIK 108
 QY 63 SSGSGSGDFTLTISRLEPEDFAVYQCYGNSRWFQGGTKVEIK 107

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 ID US-08-474-040-86 STANDARD: PRT: 108 AA.
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 XX 01-JAN-1900
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 DE Sequence 86, Application US/08474040.
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 CC Sequence 86, Application US/08474040
 CC Patent No. 5693761
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: CO, Man Sung
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: LANDOLFI, Nicholas F.
 CC APPLICANT: COELINGH, Kathleen L.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/474,040
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA; 11590 MW; 64079 CN;

Query Match 89.9%; Score 685; DB 7; Length 108;
Best Local Similarity 92.4%; Pred No 1.80e-45;
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 LTQSPGTLSPGERATLSCPASQSVSSGVLGMYQQKPGQAPRLIYGGASSRATGIPDRF 63
QY 3 LTQSPGTLSPGERATLSCPASQSVSSNLAWYQQKPGQAPRLIYGGASSRATGIPDRF 62
Db 64 SGSGSGTDFTLTISRLEPEDFAVYQCQYQYSLGRTFGQGTKEIK 108
QY 63 SGSGSGTDFTLTISRLEPEDFAVYQCQYQYSLGRTFGQGTKEIK 107

RESULT 7
ID US-07-634-278-86 STANDARD: PPT: 108 AA
XX XXXXXX
AC
XX
DT 01-JAN-1900
XX
DE Sequence 86, Application US/07634278.
XX
CC Sequence 86, Application US/07634278
CC Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA; 11590 MW; 64079 CN;

Query Match 89.9%; Score 685; DB 6; Length 108;
Best Local Similarity 92.4%; Pred No 1.80e-45;
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 LTQSPGTLSPGERATLSCPASQSVSSGVLGMYQQKPGQAPRLIYGGASSRATGIPDRF 63
QY 3 LTQSPGTLSPGERATLSCPASQSVSSNLAWYQQKPGQAPRLIYGGASSRATGIPDRF 62
Db 64 SGSGSGTDFTLTISRLEPEDFAVYQCQYQYSLGRTFGQGTKEIK 108
QY 63 SGSGSGTDFTLTISRLEPEDFAVYQCQYQYSLGRTFGQGTKEIK 107

RESULT 8
ID US-08-487-200-86 STANDARD: PPT: 108 AA
XX XXXXXX
AC
XX
DT 01-JAN-1900
XX
DE Sequence 86, Application US/08487200.
XX
CC Sequence 86, Application US/08487200
CC Patent No. 5693762
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US

CC ZIP: 94301.
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/487,200
CC FILING DATE: 7-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002610
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 86:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 108 AA; 11590 MW; 64079 CN;

Query Match 89.9%; Score 585; DB 7; Length 108;
Best Local Similarity 92.4%; Pred. No. 1.80e-45;
Matches 97; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 LTQSPGTLSPGERATLSCPASQSVSSNYLAWYQCGAPPLIYGASSPATGIPDRF 63
QY 3 LTQSPGTLSPGERATLSCPASQSVSSNYLAWYQCGAPPLIYGASSPATGIPDRF 62
Db 64 SGGSGGTDFTLTISRLEPEDFAVYQCGYGLGRFTGGTKVEIK 108
QY 63 SGGSGGTDFTLTISRLEPEDFAVYQCYLGNRPWTFGGTKVEIK 107

RESULT 9
ID PCT-US95-08743-99 STANDARD; PRT: 108 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 99, Application PC/TUS9508743.
XX
CC Sequence 99, Application PC/TUS9508743
CC GENERAL INFORMATION:

CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM: disk
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (FPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743

CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11738 MW; 63142 CN;
Query Match 89.8%; Score 684; DB 13; Length 108;
Best Local Similarity 88.7%; Pred. No. 2.17e-45;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Db 1 ELTQSPGTLSPGERATLSCRAQGSISNNYLAWYQKPGAPPLIYGASNPATGIPDR 60
QY 2 ELTQSPGTLSPGERATLSCPASQSVSSNYLAWYQCGAPPLIYGASSPATGIPDR 61
Db 61 FSGSGGTDFTLTISRLEPEDFAVYQCGYGTSPYTFGGTQIDIK 106
QY 62 FSGSGGTDFTLTISRLEPEDFAVYQCYLGNRPWTFGGTKVEIK 107
RESULT 10
ID US-08-276-852-99 SIAMIAFU; PRT: 108 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 99, Application US/08276852.
XX
CC Sequence 99, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SC1452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937

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CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11738 MW; 63142 CN;

Query Match      89.8%; Score 684; DB 7; Length 108;
Best Local Similarity 88.7%; Pred. No. 2.17e-45;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGERATLSRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 106
QY 2 ELTQSPGTLSPGERATLSRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 107
Db 61 FSGSGSGTDTLTISRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 106
QY 62 FSGSGSGTDTLTISRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 107

RESULT 11
ID PCT-US93-08786-23 STANDARD: PPT: 109 AA
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 23, Application PC/TUS9308786.
XX
CC Sequence 23, Application PC/TUS9308786
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R.
CC APPLICANT: Barbas, III, Carlos F.
CC APPLICANT: Chanock, Robert M.
CC APPLICANT: Murphy, Brian R.
CC APPLICANT: Crowe, Jr., James E.
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO RESPIRATORY SYNCYTIAL VIRUS
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East, Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08786
CC FILING DATE: 16-SEP-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Wetherell, Jr., Ph.D., John R.
CC REGISTRATION NUMBER: 31,678
CC REFERENCE/DOCKET NUMBER: FD-2791
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 23:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: rsv 6L 11L 21L; anad 221

CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 99:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 108 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 108 AA; 11738 MW; 63142 CN;

Query Match      89.8%; Score 684; DB 7; Length 108;
Best Local Similarity 88.7%; Pred. No. 2.17e-45;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 ELTQSPGTLSPGERATLSRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 106
QY 2 ELTQSPGTLSPGERATLSRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 107
Db 61 FSGSGSGTDTLTISRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 106
QY 62 FSGSGSGTDTLTISRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 107

RESULT 12
ID PCT-US95-08743-147 STANDARD: PPT: 109 AA
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 147, Application PC/TUS9508743.
XX
CC Sequence 147, Application PC/TUS9508743
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 147:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 109 AA; 11779 MW; 65550 CN;

Query Match      89.2%; Score 680; DB 13; Length 109;
Best Local Similarity 91.6%; Pred. No. 4.55e-45;
Matches 98; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Db 2 AELTQSPGTLSPGERATLSRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 61
QY 1 AELTQSPGTLSPGERATLSRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 60
Db 62 RFSGSGSGTDTLTISRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 107
QY 61 RFSGSGSGTDTLTISRLEPEDFAVYCCQYGTSPYFGQGTOLDIK 107

RESULT 13
ID US-08-276-852-147 STANDARD: PPT: 109 AA
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 147, Application US/082768e2
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XX Sequence 147, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 147:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 109 AA: 11779 MW; 65550 CN;
Query Match 89.2%; Score 680; DB 7; Length 109;
Best Local Similarity 91.6%; Pred. No. 4.55e-45;
Matches 98; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
Db 2 AELTQSPGTLSPGERATLSGRASQSVSSNYLAWYQKPGQAPRLIYGASNRATGIPD 61
QY 1 AELTQSPGTLSPGERATLSGRASQSVSSNYLAWYQKPGQAPRLIYGASNRATGIPD 60
Db 62 RFSGSGGTDFTLTISRLEPEDFAVYCYQYQYGGSG-TFGQGTKEIK 107
QY 61 RFSGSGGTDFTLTISRLEPEDFAVYCYQYQYGGSG-TFGQGTKEIK 107
RESULT 14
ID PCT-US95-08743-100 STANDARD: PRT: 104 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 100, Application PC/TUS9508743.
XX
CC Sequence 100, Application PC/TUS9508743
CC GENERAL INFORMATION:

CC APPLICANT:
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPC)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/08743
CC FILING DATE: 11-JUL-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/276,852
CC FILING DATE: 18-JUL-1994
CC INFORMATION FOR SEQ ID NO: 100:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 104 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 104 AA: 11367 MW; 58892 CN;
Query Match 87.9%; Score 670; DB 13; Length 104;
Best Local Similarity 90.3%; Pred. No. 2.90e-44;
Matches 93; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
Db 1 QSPGTLSPGERATLSGRASQSVSSNYLAWYQKPGQAPRLIYGASNRATGIPRFSG 60
QY 5 QSPGTLSPGERATLSGRASQSVSSNYLAWYQKPGQAPRLIYGASNRATGIPRFSG 64
Db 61 GSGGTDFTLTISRLEPEDFAVYCYQYQYGGSG-TFGQGTKEIK 103
QY 65 GSGGTDFTLTISRLEPEDFAVYCYQYQYGGSG-TFGQGTKEIK 107
RESULT 15
ID US-08-276-852-100 STANDARD: PRT: 104 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 100, Application US/08276852.
XX
CC Sequence 100, Application US/08276852
CC Patent No. 5652138
CC GENERAL INFORMATION:
CC APPLICANT: Burton, Dennis R
CC APPLICANT: Barbas, Carlos F
CC APPLICANT: Lerner, Richard A
CC TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
CC TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CC NUMBER OF SEQUENCES: 170
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: The Scripps Research Institute, Office of
CC ADDRESSEE: Patent Counsel
CC STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CC CITY: La Jolla
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92037
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/276,852
CC FILING DATE: 18-JUL-1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/178,302
CC FILING DATE: 30-SEP-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/954,148
CC FILING DATE: 30-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fitting, Thomas
CC REGISTRATION NUMBER: 34,163
CC REFERENCE/DOCKET NUMBER: SCRI452P
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-554-2937
CC TELEFAX: 619-554-6312
CC INFORMATION FOR SEQ ID NO: 147:
CC LENGTH: 109 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 109 AA: 11779 MW; 65550 CN;
Query Match 89.2%; Score 680; DB 7; Length 109;
Best Local Similarity 91.6%; Pred. No. 4.55e-45;
Matches 98; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
Db 2 AELTQSPGTLSPGERATLSGRASQSVSSNYLAWYQKPGQAPRLIYGASNRATGIPD 61
QY 1 AELTQSPGTLSPGERATLSGRASQSVSSNYLAWYQKPGQAPRLIYGASNRATGIPD 60
Db 62 RFSGSGGTDFTLTISRLEPEDFAVYCYQYQYGGSG-TFGQGTKEIK 107
QY 61 RFSGSGGTDFTLTISRLEPEDFAVYCYQYQYGGSG-TFGQGTKEIK 107
RESULT 14
ID PCT-US95-08743-100 STANDARD: PRT: 104 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 100, Application PC/TUS9508743.
XX
CC Sequence 100, Application PC/TUS9508743
CC GENERAL INFORMATION:

CC APPLICATION NUMBER: US 08/178,302
 CC FILING DATE: 30-SEP-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/954,148
 CC FILING DATE: 30-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Fitting, Thomas
 CC REGISTRATION NUMBER: 34,163
 CC REFERENCE/DOCKET NUMBER: SC1452P
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-554-2937
 CC TELEFAX: 619-554-6312
 CC INFORMATION FOR SEQ ID NO: 100:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 104 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 104 AA: 11367 MW: 58892 CN;
 SQ
 Query Match 87.9%; Score 670; DB 7; Length 104;
 Best Local Similarity 90.3%; Pred. No. 2.90e-44;
 Matches 93; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 Db 1 QSPGTLSPGERATLSCRASQSLNNYLAWYQKPGQAPRLIYSSSTRATGIPDRFSG 60
 QY 5 QSPGTLSPGERATLSCRASQSVSSNYLAWYQQRPGQAPRLIYGASSRATGIPDRFSG 64
 Db 61 GSGGDTFTLTISRLEPEDFVYVYQQYQNSVYTFQGQTKLEIK 103
 QY 65 GSGGDTFTLTISRLEPEDFVYVYQYQYQNSRWTFQGQTKVEIK 107

Search completed: Tue Feb 24 07:44:57 1998
 Job time : 13 secs.

W P S R E H

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:18:21 1998. MasPar time 6.66 seconds

Tabular output not generated. 223,141 Million cell updates/sec

Title: >US-08-844-215-8

Description: (1-107) from US08844215.pep

Perfect Score: 762

Sequence: 1 AELTSPGTLSTLSPGFRATL QQLYNSPWTFGQIKVEIK 107

Scoring table: PAM 150

Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq30

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 29.906; Variance 166.360; scale 0.180

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	697	91.5	108	10	Anti-HIV gp120 immuno	1.57e-42
2	697	91.5	108	19	VL region of HIV neut	1.57e-42
3	694	91.1	129	7	VL region of HIV neut	2.54e-42
4	685	89.9	107	10	Anti-HIV gp120 immuno	1.25e-41
5	685	89.9	107	19	VL region of HIV neut	1.25e-41
6	684	89.8	108	19	VL region of HIV neut	1.50e-41
7	684	89.8	108	9	Anti-HIV gp120 immuno	1.50e-41
8	684	89.8	109	10	Light chain of Amb al	1.50e-41
9	683	89.6	109	9	HSV glycoprotein F b1	1.78e-41
10	680	89.2	109	19	VL of Fab, DL 41 19,	3.00e-41
11	680	89.2	109	10	Anti-HIV gp41 immunog	3.00e-41
12	673	88.3	107	7	Human lambda light ch	1.01e-40
13	670	87.9	104	19	VL region of HIV neut	1.70e-40
14	670	87.9	104	9	Anti-HIV gp120 immuno	1.70e-40
15	670	87.9	111	19	VL of Fab, GL 41 1, b	1.70e-40
16	670	87.9	111	10	Anti-HIV gp41 immunog	1.70e-40
17	662	86.9	108	19	VL region of HIV neut	6.78e-40
18	662	86.9	129	7	VL of rearranged varia	6.79e-40
19	660	86.6	214	19	Ulcerative colitis-as	9.59e-40
20	659	86.5	129	7	F105VK-F105JK	1.14e-39

21	656	86.1	107	10	R54308	Anti-HIV gp120 immuno	1.92e-39
22	656	86.1	107	19	W01266	VL region of HIV neut	1.92e-39
23	656	86.1	134	20	W11555	Anti-lung tumour anti	1.92e-39
24	655	86.0	108	10	P54263	Anti-HIV gp120 immuno	2.28e-39
25	652	85.6	134	22	W24539	Immunoglobulin r101-2	3.89e-39
26	652	85.6	215	19	W07616	Ulcerative colitis-as	3.83e-39
27	641	84.1	108	10	R54255	Anti-HIV gp120 immuno	2.57e-38
28	641	84.1	108	19	W01275	VL region of HIV neut	2.57e-38
29	641	84.1	109	9	P50218	HSV glycoprotein F b1	2.57e-38
30	636	83.5	108	19	W01267	VL region of HIV neut	6.10e-38
31	628	82.4	107	10	P54265	Anti-HIV gp120 immuno	2.43e-37
32	628	82.4	107	19	W01297	VL region of HIV neut	2.43e-37
33	626	82.2	100	5	P25324	VL region of human rh	3.44e-37
34	626	82.2	112	10	P54279	Anti-HIV gp41 immunog	3.44e-37
35	626	82.2	112	19	W01294	VL of Fab, SS 41 8, b	3.44e-37
36	625	82.0	116	11	K62830	Human V-kappa vk65.8	4.09e-37
37	625	82.0	116	20	R03948	DNA fragment vk65.8,	4.09e-37
38	625	82.0	116	7	R38650	Human V-kappa fragmen	4.09e-37
39	623	81.8	108	10	P54309	Anti-HIV gp120 immuno	5.78e-37
40	623	81.4	107	19	W01294	VL region of HIV neut	5.78e-37
41	620	81.4	107	9	P54325	Anti-HIV gp120 immuno	9.70e-37
42	620	81.4	107	19	W01295	VL region of HIV neut	9.70e-37
43	618	81.1	104	19	W01271	VL region of HIV neut	1.37e-36
44	618	81.1	104	9	R54313	Anti-HIV gp120 immuno	1.37e-36
45	617	81.0	107	9	R54326	Anti-HIV gp120 immuno	1.53e-36

ALIGNMENTS

RESULT 1
ID R54307 standard; protein; 108 AA.
AC R54307;
DE 10-NOV-1994 (first entry)
DE Anti-HIV gp120 immunoglobulin light chain variable region b24.
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region.
OS Homo sapiens

FT Key Location/Qualifiers

FT Region 1..21

FT /label= FR1

FT Region 22..33

FT /label= CDR1

FT Region 34..48

FT /label= FR2

FT Region 49..55

FT /label= CDR2

FT Region 56..87

FT /label= FR3

FT Region 88..95

FT /label= CDR3

FT Region 97..108

FT /label= FR4

FN W9407922-A.

PD 14-APR-1994.

PF 30-SEP-1993. U993328.

PR 30-SEP-1992; US-954148.

PA (SCRI) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

DI WPI: 94-135516/16.

PT New human monoclonal antibodies neutralising HIV - react with

PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo

PT or in vitro diagnosis and for passive immuno-therapy

PS Example, Page 177-178, 248pp, English.

CC Lymphocyte mRNA was converted to cDNA and subjected to PCR

CC amplification using primers specific for heavy and light chain

CC variable regions. The amplification products were inserted into a

CC di-electronic vector to produce a library of fragments. E.coli XLI

CC Blue cells were transformed with the library. Filamentous phage were

CC produced which expressed the MAB regions on their surface. Panning

CC with gp120 and gp41 resulted in the recovery of immunoreactive

CC clones. The light chain VK region sequence p54307 is from a gp120-

CC specific clone.

SQ Sequence 108 AA:

Query Match 91.5%: Score 697; DB 10; Length 108;
 Best Local Similarity 92.5%: Pred. No. 1.57e-42;
 Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 eltspsgtlslsperatlscrasqvisnlyawyyqkqpgqaprllygvsnratgipdr 60
 |||||
 QY 2 ELTOSPGTSLSPGERATLSRASQVSNNYLAWYQQPQAPRLIYGASSPATGIPDP 61
 |||||
 Db 61 fsgsgsgtdftltisrlepedfavyycqygtspwtfgggtkveik 106
 |||||
 QY 62 FSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRWTFGGQTKVEIK 107
 |||||

RESULT 2

ID W01265 standard; Protein; 108 AA.

DT 28-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAb, clone b24.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN W09602273-A1.
 PD 03-DEC-1996.

PF 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCR1) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner PA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection.
 PS Example; Fig 11; 366pp: English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JKI
 CC gene clone, b24. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection
 SQ Sequence 108 AA;

Query Match 91.5%: Score 697; DB 19; Length 108;
 Best Local Similarity 92.5%: Pred. No. 1.57e-42;
 Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 eltspsgtlslsperatlscrasqvisnlyawyyqkqpgqaprllygvsnratgipdr 60
 |||||
 QY 2 ELTOSPGTSLSPGERATLSRASQVSNNYLAWYQQPQAPRLIYGASSPATGIPDP 61
 |||||
 Db 61 fsgsgsgtdftltisrlepedfavyycqygtspwtfgggtkveik 106
 |||||
 QY 62 FSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRWTFGGQTKVEIK 107
 |||||

RESULT 3

ID R38672 standard; Protein; 129 AA.

AC R38672;
 DT 01-NOV-1993 (first entry)
 DE VK325-JK2.
 KW Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4 receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= sig_peptide
 FT Protein 21..129
 FT /label= mat_protein
 FT Region 1..116
 FT /label= vk325
 FT Region 117..129
 FT /label= JK2
 FT Region 44..55
 FT /label= CDR1
 FT Region 71..77
 FT /label= CDR2
 FT Region 110..117
 FT /label= CDR3

FT Misc-difference 1
 FT /note= "Met encoded by ATC (sic)"
 FT Misc-difference 35
 FT /note= "Pro encoded by GCA (sic)"
 FT Misc-difference 99
 FT /note= "Leu encoded by GTG (sic)"
 FT Misc-difference 113
 FT /note= "Gly encoded by GAT (sic)"
 FT Misc-difference 114
 FT /note= "Ser encoded by AAC (sic)"
 FT Misc-difference 116
 FT /note= "Pro encoded by GTT (sic)"
 PN W09312232-A.
 PD 24-JUN-1993.
 PF 10-DEC-1992; U10928.
 PR 10-DEC-1991; US-804652.
 PA (DAND) DANA FARRER CANCER INST INC
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
 DR WPI: 93-214174/26.
 DR N-PSDB: Q42706.
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Disclosure: Page 74-75; 109pp: English.
 CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from
 CC other F105 VK sequences given elsewhere in the specification) was
 CC compared with germline gene Humvk325 (Q42706), showing 97.7%
 CC similarity. By nucleotide sequence analysis, F105 appears to
 CC be derived from a member of the VK III subgroup gene family.
 SQ Sequence 129 AA;

Query Match 91.1%: Score 694; DB 7; Length 129;
 Best Local Similarity 93.3%: Pred. No. 2.54e-42;
 Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 24 ltsgptslsperatlscrasqvisnlyawyyqkqpgqaprllygvsnratgipdr 83
 |||||
 QY 3 LTGSPGTSLSPGERATLSRASQVSNNYLAWYQQPQAPRLIYGASSPATGIPDP 82
 |||||

Db 84 ssgsgsgtdftltisrlepedfavyycqygtspwtfgggtkveik 128
 |||||
 QY 63 SSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRWTFGGQTKVEIK 107
 |||||

RESULT 4

ID R54311 standard; protein; 107 AA.

```

AC * R54311;
DE 10-NOV-1994 (first entry)
KW Anti-HIV gp120 immunoglobulin light chain variable region B20.
KW Human immunodeficiency virus: HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain;
KW variable region; framework; complementarity determining region
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..95
FT /label= CDR3
FT Region 97..107
FT /label= FR4
FT Region 108..110
FT /label= FR5
PN WO9407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCRI ) SCRIpps RES INST
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 94-135516/15.
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 180: 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC diazotronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence R54311 is from a gp120-
CC specific clone
SQ Sequence 107 AA;

Query Match 89.9%; Score 685; DB 10; Length 107;
Best Local Similarity 89.6%; Prod No 1 25e-41;
Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Db 1 eltsqptslsperatlscrasqslsnnylawyqgkqgqaprllygsstrgtgipdr 60
QY 2 ELTOSPTLSLSPGEPATLSCPASQSVSSNYLAWYQCPPTCAPPLLIYGASSPATGIPDR 61
Db 61 fsggsgtdftltisrlepedfavyycqhygnsvytfgqgtkleik 106
QY 62 FSGSGSGTDFLTLSRLEPEDFAVYVCQLYGNRWTFGQGTKEIK 107

RESULT 5
ID WO1269 standard; Protein; 107 AA.
AC WO1269;
DE 28-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone B20.
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
FT Region 109..110
FT /label= FR5
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.

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FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88 96
FT /label= CDR3
FT Region 98..107
FT /label= FR4
FT Region 108..110
FT /label= FR5
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCRI ) SCRIpps RES INST
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example: Fig 11: 366pp; English.
CC The sequences given in WO1261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC binds mature gp120 preferentially over the precursor gp160. The MAB
CC may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 107 AA;

Query Match 89.9%; Score 685; DB 19; Length 107;
Best Local Similarity 89.6%; Prod No 1 25e-41;
Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Db 1 eltsqptslsperatlscrasqslsnnylawyqgkqgqaprllygsstrgtgipdr 60
QY 2 ELTOSPTLSLSPGEPATLSCPASQSVSSNYLAWYQCPPTCAPPLLIYGASSPATGIPDR 61
Db 61 fsggsgtdftltisrlepedfavyycqhygnsvytfgqgtkleik 106
QY 62 FSGSGSGTDFLTLSRLEPEDFAVYVCQLYGNRWTFGQGTKEIK 107

RESULT 6
ID WO1278 standard; Protein; 108 AA.
AC WO1278;
DE 29-JAN-1997 (first entry)
DE VL region of HIV neutralising MAB, clone b6.
KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..96
FT /label= CDR3
FT Region 97..108
FT /label= FR4
FT Region 109..110
FT /label= FR5
PN WO9602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.

```

PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner PA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection
 PS Example; Fig 11: 36pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, b6. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/mL, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 108 AA;

Query Match 89.8%; Score 684; DB 19; Length 108;
 Best Local Similarity 88.7%; Pred. No. 1.50e-41;
 Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltspgtltslsperatlscragqssnylawyqgkpgqaprllyqasnratgipdr 60
 QY 2 ELTQSPGTLTSLSPGERATLSCRASQSVSSNYLAWYQGPQAPRLLIYGASSRATGIPDR 61
 Db 61 fsgsgsgtdftltisrlepedfavyycqgqytsptfsggtqldik 106
 QY 62 FSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSRWTFGGQTKVEIK 107

RESULT 7
 ID R54316 standard; protein; 108 AA.
 AC R54316;
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain variable region b6.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..21
 FT /label= FR1
 FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..96
 FT /label= CDR3
 FT Region 97..108
 FT /label= FR4
 PN W09407922-A.
 PD 14-APR-1994.
 PF 30-SEP-1993; U09328.
 PR 30-SEP-1992; US-954148.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner PA;
 DR WPI: 94-135516/16.
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them; useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Example; Page 186: 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive

CC clones. The light chain VK region sequence R54316 neutralises HIV1
 CC gp120
 SQ Sequence 108 AA;

Query Match 89.8%; Score 684; DB 9; Length 108;
 Best Local Similarity 88.7%; Pred. No. 1.50e-41;
 Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 eltspgtltslsperatlscragqssnylawyqgkpgqaprllyqasnratgipdr 60
 QY 2 ELTQSPGTLTSLSPGERATLSCRASQSVSSNYLAWYQGPQAPRLLIYGASSRATGIPDR 61
 Db 61 fsgsgsgtdftltisrlepedfavyycqgqytsptfsggtqldik 106
 QY 62 FSGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSRWTFGGQTKVEIK 107

RESULT 8
 ID R56286 standard; protein; 109 AA.
 AC R56286;
 DT 04-MAR-1995 (first entry)
 DE Light chain of Amb al-specific IgG4 antibody.
 KW Allergen-specific immunoglobulin A; IgA; AL 15-5.2; light chain;
 KW allergen Amb a 1; ragweed; Ambrosia elator.
 OS Synthetic.
 PN W09414475-A.
 PD 07-JUL-1994.
 PF 20-DEC-1993; W12501
 PR 21-DEC-1992; US-994126.
 PA (TANO-) TANOX BIOSYSTEMS INC.
 PI Chang TW;
 DR WPI: 94-234353/28.
 DR N-PSDB; Q66538.
 PT Compsn. contg. allergen specific IgA for treating mucosal tissue
 PT - and conjugates of allergen specific Ig with polymer, for
 PT treating IgE mediated allergies and for isolation of specific
 PT allergens
 PS Example; Page 27-28: 36pp; English.
 CC Blood samples were collected from patients immunised with allergens
 CC including ragweed (Ambrosia elator) extracts. The dominant allergen
 CC in short ragweed is Amb a 1. Purified PBLs were immortalised and
 CC then fused with mouse myeloma cell line 653 and the resultant clones
 CC were screened using Amb a 1 protein. A single cell subclone AL 16-5.2,
 CC secreting Amb al-specific IgG4, kappa antibody was selected. Total
 CC RNA was prepd. from the AL 16-5.2 cells and first strand cDNA was
 CC pred. using oligo dT primers. When the first strand cDNA was used as
 CC the template, and the 5' and 3' kappa light chain primers (Q66540,
 CC Q66541) were used in PCR and amplified band of the expected size was
 CC noted. The DNA sequence of several subclones contg. this amplified
 CC DNA fragment was determined. The sequence and its deduced AA
 CC sequence are shown in Q66538 and R56286. Comparison of the deduced
 CC AL 16-5.2 L-chain sequence with human V region sequences indicates
 CC that it is a member of the human VK III subgp.
 SQ Sequence 109 AA;

Query Match 89.8%; Score 684; DB 10; Length 109;
 Best Local Similarity 87.6%; Pred. No. 1.50e-41;
 Matches 92; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Db 4 ltsqptltslsperatlscragqssnylawyqgkpgqaprllyqasnratgipdr 63
 QY 3 LTQSPGTLTSLSPGERATLSCRASQSVSSNYLAWYQGPQAPRLLIYGASSRATGIPDR 62
 Db 64 tsgsgsgtdftltisrlepedfavyycqgqfnsqwtfgggtkveik 108
 QY 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRSRWTFGGQTKVEIK 107

RESULT 9
 ID R50217 standard; protein; 109 AA.
 AC R50217;
 DT 31-OCT-1994 (first entry)
 DE HSV glycoprotein F binding MAB clone rsv6/11/21/22L VH/VL domain.

KW Complementarity determination region: CDR3: human; bronchiolitis;
 KW monoclonal antibody; epitope: glycoprotein F; influenza virus;
 KW respiratory syncytial virus; RSV; disease: rhinovirus; coronavirus;
 OS lung; pneumonia;
 OS Synthetic.

FT Key Location/Qualifiers
 FT Region 1..23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57
 FT /label= CDR2
 FT Region 58..89
 FT /label= FR3
 FT Region 90..97
 FT /label= CDR3
 FT Region 98..109
 FT /label= FR4
 PN WO9406448-A.
 PD 31-MAR-1994.
 PF 16-SEP-1993: U08786.
 PR 16-SEP-1992: US-945515.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Barbas CF, Burton DR, Chanock PM, Crowe JE, Murphy RP,
 DR WPI: 94-118147/14.
 PT Human neutralising monoclonal antibodies to respiratory syncytial
 PT virus - for treatment prophylaxis and diagnosis of PSV and other
 PT diseases of the respiratory tract
 PS Disclosure: Fig 4: 104pp; English.
 CC The sequences given in R50215-19 represent the heavy and light chain
 CC variable domains of various clones of a human monoclonal antibody
 CC which binds to an epitope on glycoprotein F of respiratory syncytial
 CC virus (RSV). These antibodies may be used as a reagent for the
 CC diagnosis of RSV disease and other viral mucosal diseases, eg.
 CC influenza virus, rhinovirus and coronavirus. They are particularly
 CC useful in ameliorating RSV when delivered directly to the lungs, and
 CC may also be used for treating pneumonia and bronchiolitis.
 SQ Sequence 109 AA;

Query Match 89.6%; Score 683; DB 9; Length 109;
 Best Local Similarity 89.7%; Pred. No. 1.78e-41;
 Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 2 aeltspgtlslspgeratlsratqssnylawyqgqgqprlllycasratdipd 61
 QY 1 AELTQSPGTLSLSPGERATLSRATQSSVSSNYLAWYQGRPQAPRLIYGASSRATGIPD 60
 Db 62 rfsqsgtdftltisrlepedfamyvqdydispytfgggtkveik 108
 QY 61 RFSGSGTDTFTLSRLEPEDFAVYVCQLYGNRSRWTFGGKTVEIK 107

RESULT 10
 ID WO1320 standard: Protein: 109 AA.

AC WO1320:
 DE 29-JAN-1997 (first entry)
 DE VL of Fab, DL 41 19, binds to HIV gp41.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp150; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FH Region 1..23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57

FT /label= CDR2
 FT Region 58 89
 FT /label= FR3
 FT Region 90 97
 FT /label= CDR3
 FT Region 98..109
 FT /label= FR4
 PN WO9602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995: U08743.
 PR 18-JUL-1994: US-276852
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection.
 PS Example 1: Fig 19: 35pp; English.
 CC The sequences given in WO1320-24 represent the light chain variable
 CC regions (VH) of a series of antibody fragments (FAB's) which are
 CC immunoreactive with HIV glycoprotein gp41. This sequence represents
 CC the sequence of the clone, DL 41 19. These sequences represent light
 CC chains which bind to the heavy light chain clones given in WO1315-19. A
 CC monoclonal antibody containing one of these Fab sequences may have the
 CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity
 CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.
 CC The MAb may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 109 AA;

Query Match 89.2%; Score 680; DB 19; Length 109;
 Best Local Similarity 91.6%; Pred. No. 3.00e-41;
 Matches 98; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Db 2 aeltspgtlslspgeratlsratqssnylawyqgqgqprlllycasratdipd 61
 QY 1 AELTQSPGTLSLSPGERATLSRATQSSVSSNYLAWYQGRPQAPRLIYGASSRATGIPD 60
 Db 62 rfsqsgtdftltisrlepedfamyvqdydispytfgggtkveik 107
 QY 61 RFSGSGTDTFTLSRLEPEDFAVYVCQLYGNRSRWTFGGKTVEIK 107

RESULT 11
 ID R54275 standard: protein: 109 AA.

AC R54275;
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp41 immunoglobulin light chain V region clone DL 41 19.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
 KW neutralisation; monoclonal antibody; light chain; variable region;
 KW framework region; complementarity determining region.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FH Region 1..23
 FT /label= FR1
 FT Region 24..35
 FT /label= CDR1
 FT Region 36..50
 FT /label= FR2
 FT Region 51..57
 FT /label= CDR2
 FT Region 58..89
 FT /label= FR3
 FT Region 90..97
 FT /label= CDR3
 FT Region 98..109
 FT /label= FR4
 PN WO9407923-A.
 PD 14-APR-1994.
 PR 30-SEP-1993: U09328.
 PR 30-SEP-1992: US-954148.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 94-135516/16.

PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS Claim 11; Page 215-216; 248pp; English.
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC B cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAB regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VL region sequence R54275 neutralises HIV1
 CC gp41.
 SQ Sequence 109 AA;

Query Match 89.2%; Score 680; DB 10; Length 109;
 Best Local Similarity 91.6%; Pred. No. 3,00e-41;
 Matches 98; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Db 2 aeltspgtlslspgervivscrasqsvssnylawyqkpgqaprllygassnatratgipd 61
 QY 1 aeltspgtlslspgervivscrasqsvssnylawyqkpgqaprllygassnatratgipd 60
 Db 62 rfsgsgtdftltisrlepedfavyycqygsgg-tfgggtkveik 107
 QY 61 pfsgsgtdftltisrlepedfavyycqygsgg-tfgggtkveik 107

RESULT 12
 ID R38593 standard; peptide; 107 AA.
 AC R38593;
 DT 28-OCT-1993 (first entry)
 DE Human lambda light chain subgroup 3 (hL3).
 KW Antibody; variable domain; light; L; heavy; H; consensus;
 KW affinity; antigen; immunogenicity; humanisation; framework.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 96
 FT /note="residue conserved in less than 50% of the
 FT known sequences of hL3"
 FT WO9311794-A.
 PD 24-JUN-1993.
 PF 14-DEC-1992; U10906.
 PR 13-DEC-1991; US-808464.
 PA (XOMA) XOMA CORP.
 PI Fishwild DM, Kohn FR, Little RG, Studnicka GM;
 DR WPI; 93-213827/26.
 CC Antibodies prepn. used for treatment of auto-immune diseases - by
 PT replacement of critical residues to reduce immunogenicity but
 PT retain binding affinity, etc.
 PS Claim 2; Page 93-94; 160pp; English.
 CC The consensus amino acid sequences for the subgroups of light
 CC chains (hK1 - R38590, hK3 - NGK, hK2 - GST, hL1 - R38591, hL2 -
 CC R38592, hL3 - R38593, hL5 - R38594, hK4 - R38595, hL4 - R38596,
 CC and hL5 - R38597) and heavy chains (hH3 - R38598, hH1 - R38599 and
 CC hH2 - R38600) of human variable domains may be used to prepare, for
 CC example, a modified mouse antibody variable domain that retains the
 CC affinity of the natural domain for antigen while exhibiting reduced
 CC immunogenicity in humans.
 CC Unlike other methods of humanisation, which advocate the
 CC replacement of entire antibody framework regions with those of human
 CC antibodies, this method involves only the introduction of human
 CC residues into those positions not critical for antigen binding.
 CC This ensures that the binding properties of the modified antibody
 CC are not diminished.
 SQ Sequence 107 AA;

Query Match 88.3%; Score 673; DB 7; Length 107;
 Best Local Similarity 92.4%; Pred. No. 1.01e-40;
 Matches 97; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Db 4 ltqspgtlslspgervivscrasqsvss-ylawyqkpgqaprllygassnatratgipd 62
 QY 1 ltqspgtlslspgervivscrasqsvss-ylawyqkpgqaprllygassnatratgipd 61

QY 3 LIQSPGTLSPGKATLSCKASQSVSSNYLAWYQKPGQAPRLLYGASSKAIGIPDRF 62
 Db 63 ssgsgtdftltisrlepedfavyycqygsggxtfqqgtdveik 107
 QY 63 SGSGSGTDFTLTISRLEPEDFAVYCYQLYGNRPWTFGGGTKEIK 107

RESULT 13
 ID W01279 standard; protein; 104 AA.
 AC W01279;
 DT 29-JAN-1997 (first entry)
 DE VL region of HIV neutralising MAB, clone s6.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..18
 FT /label= FR1
 FT Region 19..30
 FT /label= CDR1
 FT Region 31..45
 FT /label= FR2
 FT Region 46..52
 FT /label= CDR2
 FT Region 53..84
 FT /label= FR3
 FT Region 85..93
 FT /label= CDR3
 FT Region 94..104
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996.
 PF 11-JUL-1995; 008743.
 PR 18-JUL-1994; US-276852.
 PA (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI; 96-179601/18.
 PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
 PT passive immuno-therapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 CC The sequences given in W01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, s6. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The MAB
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 104 AA;

Query Match 87.9%; Score 670; DB 19; Length 104;
 Best Local Similarity 90.3%; Pred. No. 1.70e-40;
 Matches 93; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 1 qspgtlslspgervivscrasqsvssnylawyqkpgqaprllygassnatratgipd 60
 QY 5 QSPGTLSLSPGKATLSCKASQSVSSNYLAWYQKPGQAPRLLYGASSPATRIPDPFSG 64
 Db 61 gsgsgtdftltisrlepedfavyycqygsggxtfqqgtdveik 103
 QY 65 SGSGTDFTLTISRLEPEDFAVYCYQLYGNRPWTFGGGTKEIK 107

RESULT 14
 ID R54317 standard; protein; 104 AA.
 AC R54317;
 DT 10-NOV-1994 (first entry)
 DE Anti-HIV gp120 immunoglobulin light chain variable region s6.
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;

```

KW neutralisation: monoclonal antibody: kappa light chain;
KW variable region: framework: complementarity determining region
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..18
FT /label= FR1
FT Region 19..30
FT /label= CDR1
FT Region 31..45
FT /label= FR2
FT Region 46..52
FT /label= CDR2
FT Region 53..84
FT /label= FR3
FT Region 85..93
FT /label= CDR3
FT Region 94..104
FT /label= FR4
FT W09407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCR1 ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA:
DR WPI: 94-13515/16
PT New human monoclonal antibodies neutralising HIV - react with
PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT or in vitro diagnosis and for passive immuno-therapy
PS Example: Page 186-187; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which were screened with the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The light chain VK region sequence R54317 neutralises HIV1
CC gp120.
SQ Sequence 104 AA:

Query Match 87.9%; Score 670; DB 9; Length 104;
Best Local Similarity 90.3%; Pred No 170e-40;
Matches 93; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 1 qspgtlslspgeratlscrasgysnnylawyqgkpgqaprllygsstratgipdrfsq 60
   |||||
QY 5 QSPGTLSPGERATLSCRASQSVSSNYLAWYQRPQAPRLLYGASSTRATGIPDRFSG 64

Db 61 gsgtdftltisrlepedfavyycqyqnsyvtfgggtkleik 103
   :|||||
QY 65 SGSGTDFTLTISRLEPEDFAVYVCQLYGNRPWTFGGGTKEIK 107

RESULT 15
ID W01322 standard; Protein: 111 AA.
AC W01322;
DE 29-JAN-1997 (first entry)
DE VL of Fab, GL 41 1, binds to HIV gp41.
KW Heavy chain: light chain; variable region, VH, monoclonal antibody;
KW MAB: HIV; human immunodeficiency virus; glycoprotein: gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT Region 24..35
FT /label= CDR1
FT Region 36..50
FT /label= FR2
FT Region 51..57
FT /label= CDR2
FT Region 58..89

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FT /label= FR3
FT Region 90..97
FT /label= CDR3
FT Region 98..111
FT /label= FR4
PN W09602273-A1.
PD 01-FEB-1996.
PF 11-JUL-1995; U08743.
PR 18-JUL-1994; US-276852.
PA (SCR1 ) SCRIPPS RES INST.
PI Barbas CF, Burton DR, Lerner RA;
DR WPI: 96-179601/18.
PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT passive immuno-therapy and detection of HIV infection.
PS Example 3; Fig 19; 366pp; English.
CC The sequences given in W01320-24 represent the light chain variable
CC regions (VH) of a series of antibody fragments (FAB's) which are
CC immunoreactive with HIV glycoprotein gp41. This sequence represents
CC the sequence of the clone, GL 41 1. These sequences represent light
CC chains which bind to the heavy light chain clones given in W01315-19. A
CC monoclonal antibody containing one of these Fab sequences may have the
CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity
CC assay by 50 % at a concentration of less than 700 ng of antibody/ml
CC The MAB may be used for determining immunocompetence of a human anti-HIV
CC antibody and in the detection of HIV infection.
SQ Sequence 111 AA;

Query Match 87.9%; Score 670; DB 19; Length 111;
Best Local Similarity 87.9%; Pred No 1.70e-40;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

Db 2 aeltspatlslspgeratlscrasgysnnylawyqgkpgqaprllygsstratgipdr 61
   |||||
QY 1 AELTSPGTLSPGERATLSCRASQSVSSNYLAWYQRPQAPRLLYGASSTRATGIPD 60

Db 62 rfsqsgsqaadtltisrlepedfavyycqyqagsh-tfgggtkleik 107
   |||||
QY 61 RFSQSGSGTDTLTISRLEPEDFAVYVCQLYGNRPWTFGGGTKEIK 107

Search completed: Tue Feb 24 07:18:48 1998
Job time : 27 secs.

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(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:15:25 1998 MasPar time 5.77 Seconds
498,040 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-7
Description: (1-126) from US08844215.pep
Perfect Score: 949
Sequence: 1 EVQLLESGSEVKKPGSSVKV.....GSCGWEDPWWGGTLVTVSS 126

Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210988 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 41.449; Variance 70.286; scale 0.500

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	591	62.3	117	5	HV1A_HUMAN IG HEAVY CHAIN V-1 PE	1 04e-110
2	532	56.1	117	5	HV1B_HUMAN IG HEAVY CHAIN PRECUR	1 15e-96
3	515	54.3	117	5	HV1G_HUMAN IG HEAVY CHAIN PRECUR	1 21e-92
4	486	51.2	143	5	HV1C_HUMAN IG HEAVY CHAIN PRECUR	8 38e-86
5	478	50.4	125	5	HV1F_HUMAN IG HEAVY CHAIN V-1 PE	5 36e-84
6	470	49.5	114	5	HV0C_MOUSE IG HEAVY CHAIN V-1 PE	4 90e-82
7	454	47.8	140	5	HV02_MOUSE IG HEAVY CHAIN PRECUR	2 68e-78
8	445	47.0	120	5	HV03_MOUSE IG HEAVY CHAIN V-1 PE	1 98e-76
9	445	46.9	120	5	HV03_MOUSE IG HEAVY CHAIN V-1 PE	3 39e-76
10	445	46.9	139	5	HV07_MOUSE IG HEAVY CHAIN PRECUR	3 39e-76
11	441	46.5	118	5	HV01_MOUSE IG HEAVY CHAIN V-1 PE	2 90e-75
12	438	46.2	117	5	HV12_MOUSE IG HEAVY CHAIN V-1 PE	1 45e-74
13	436	45.9	117	5	HV06_MOUSE IG HEAVY CHAIN PRECUR	4 24e-74
14	435	45.8	117	5	HV05_MOUSE IG HEAVY CHAIN PRECUR	7 25e-74
15	434	45.7	117	5	HV03_MOUSE IG HEAVY CHAIN V-1 PE	1 24e-73
16	432	45.5	138	5	HV13_MOUSE IG HEAVY CHAIN PRECUR	3 62e-73
17	431	45.4	117	5	HV14_MOUSE IG HEAVY CHAIN PRECUR	6 18e-73
18	430	45.3	117	5	HV04_MOUSE IG HEAVY CHAIN PRECUR	1 06e-72
19	427	45.0	117	5	HV05_MOUSE IG HEAVY CHAIN PRECUR	5 26e-72
20	419	44.2	117	5	HV49_MOUSE IG HEAVY CHAIN PRECUR	3 79e-70
21	415	43.7	117	5	HV09_MOUSE IG HEAVY CHAIN PRECUR	3 20e-69
22	415	43.7	124	5	HV10_MOUSE IG HEAVY CHAIN V-1 PE	3 20e-69

23	414	43.6	122	5	HV1G_HUMAN IG HEAVY CHAIN V-1 PE	5 46e-69
24	408	43.0	121	5	HV01_MOUSE IG HEAVY CHAIN V-1 PE	1 34e-67
25	407	42.9	137	5	HV11_MOUSE IG HEAVY CHAIN PRECUR	2 28e-67
26	405	42.7	117	5	HV1C_MOUSE IG HEAVY CHAIN PRECUR	5 50e-67
27	404	42.6	125	5	HV1K_HUMAN IG HEAVY CHAIN V-1 PE	1 12e-66
28	401	42.3	124	5	HV1E_HUMAN IG HEAVY CHAIN V-1 PE	5 54e-66
29	400	42.1	120	5	HV3U_HUMAN IG HEAVY CHAIN V-1 PE	9 42e-66
30	399	42.0	122	5	HV3H_HUMAN IG HEAVY CHAIN V-1 PE	1 60e-65
31	393	41.4	117	5	HV3C_HUMAN IG HEAVY CHAIN PRECUR	3 87e-64
32	392	41.3	122	5	HV3A_HUMAN IG HEAVY CHAIN V-1 PE	6 58e-64
33	391	41.2	120	5	HV1H_HUMAN IG HEAVY CHAIN V-1 PE	1 12e-63
34	383	40.4	121	5	HV3J_HUMAN IG HEAVY CHAIN V-1 PE	7 42e-62
35	379	39.9	119	5	HV3I_HUMAN IG HEAVY CHAIN V-1 PE	6 40e-61
36	378	39.8	120	5	HV3E_HUMAN IG HEAVY CHAIN V-1 PE	1 08e-60
37	377	39.7	136	5	HV15_MOUSE IG HEAVY CHAIN PRECUR	1 84e-60
38	374	39.4	142	5	HV01_PAT IG HEAVY CHAIN PRECUR	8 95e-60
39	370	39.0	115	5	HV3D_HUMAN IG HEAVY CHAIN V-1 PE	7 37e-59
40	370	39.0	123	5	HV3D_MOUSE IG HEAVY CHAIN V-1 PE	7 37e-59
41	368	38.8	117	5	HV03_CAPRA IG HEAVY CHAIN PRECUR	2 11e-58
42	366	38.6	119	5	HV03_MOUSE IG HEAVY CHAIN V-1 PE	6 05e-58
43	365	38.5	119	5	HV37_MOUSE IG HEAVY CHAIN V-1 PE	1 02e-57
44	364	38.4	114	5	HV3B_HUMAN IG HEAVY CHAIN V-1 PE	1 73e-57
45	364	38.4	119	5	HV38_MOUSE IG HEAVY CHAIN V-1 PE	1 73e-57

ALIGNMENTS

RESULT 1
ID HV1A_HUMAN STANDARD: PRT: 117 AA.
AC P01742:
DT 21-JUL-1986 (REL. 01, CREATED)
DI 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-1 REGION (EU).
OS HOMO SAPIENS (HUMAN).
CC EUTRYPOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 71064024.
RA CUNNINGHAM R.A., RUTISHAUSER U., GALL W.E., GOTTlieb P.D.,
RA WAXDAL M.J., EDELMAN G.M.:
RL BIOCHEMISTRY 9:3161-3170(1970).
RN [2]
KP DISULFIDE BOND.
RX MEDLINE: 71064027.
RA GALL W.E., EDELMAN G.M.:
RA BIOCHEMISTRY 9:3188-3196(1970).
RL BIOCHEMISTRY 9:3188-3196(1970).
CC -1- THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MYELOMA PROTEIN HAS
CC ALSO BEEN DETERMINED.
DR PIR: A02023; GIHEU.
DP HSP: P01810; IFEV.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFD 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12472 MW: 10808172 CRC32:

Query Match 62.3%; Score 591; DB 5; Length 117;
Best Local Similarity 79.0%; Pred. No. 1.04e-110;
Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Db 1 gvglgsgaevkkgssvkvscasggtfarsalwvrgpaggglewmqgvlmfgppny 60
Qy 1 EVQLLESGSEVKKPGSSVKVSPFASRSGSFSYNFWVRAPGSGLEWMQJLIPEFGIAN 50
Db 61 aqkfgprtticadstntatymelsslrsestafycaggy 100
Qy 61 AOKFOGRTIITADESTATGYMELSSLRSEDTAVYVCAMPY 100

RESULT 2
ID HV1B_HUMAN STANDARD: PRT: 117 AA.


```

FT DOMAIN 99 107 D SEGMENT
FT DOMAIN 108 125 J SEGMENT
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 125 125
SQ SEQUENCE 125 AA: 13579 MW: 6745023 CRC32:

Query Match 50.4% Score 478 DB 5: Length 125;
Best Local Similarity 50.8% Pred No 5 36e-84;
Matches 68: Conservative 26; Mismatches 35; Indels 1; Gaps 1;

Db 1 qvqlqsgaeivkagssvkmcsksgyftfssygmwvkrpqgglewgiyngpqtany 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQLLESGSEVKKPGSSVKVSCPRASGSGFSPSYNFWVPQAPGQGLEWMGGIIPMFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 qprsqarftvrdstttvymelkalltsadtaiyycarg-ahysdtdtdstslgpgwqgt 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AQKFGQGVITTADESTATGYMELSLSPSEDTAVYICAMPYKHCPSGSGWGFDPWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 120 lltvss 125
:|||||:
QY 121 LVTYSS 126

RESULT 6
ID HV00_MOUSE STANDARD: PRT: 114 AA
AC P01741:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (ANTI-APSONATE ANTIBODY).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
RN EUTHERIA: RODENTIA
RN [1]
RP SEQUENCE.
RC STRAIN-A/J:
RX MEDLINE: 79195438.
FA CAPRA J D, NISONOFF A;
RL J. IMMUNOL. 123:279-284(1979).
CC -1- ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF THE IGG1
CC SURCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V REGION
CC SEQUENCE.
DR PIR: A02022; GINSA.
DR HSP: P01772; IFGV.
KW IMMUNOGLOBULIN V REGION: ANTIAPSONATE ANTIBODY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA: 12555 MW: 1A027F1D CRC32:

Query Match 49.5% Score 470; DB 5: Length 114;
Best Local Similarity 70.4% Pred No 4 80e-82;
Matches 69: Conservative 17; Mismatches 12; Indels 0; Gaps 0;

Db 1 evqlqsgaeivkagssvkmcsksgyftfssygmwvkrpqgglewgiyngpqtany 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQLLESGSEVKKPGSSVKVSCPRASGSGFSPSYNFWVPQAPGQGLEWMGGIIPMFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 aqkfgqvritadestntaymelslrsdsdtavycav 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AQKFGQGVITTADESTATGYMELSLSPSEDTAVYICAM 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
ID HV02_MOUSE STANDARD: PRT: 140 AA.
AC P01746:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
RN EUTHERIA: RODENTIA
RN [1]
RP SEQUENCE FROM N.A.

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PC STRAIN-A/J:
EX MEDLINE: 82152818.
FA SINS J, PARRITTS T H, ESTESS P, SLAUGHTER C, TUCKER P W.
RA CAPRA J D.
P1 SCIENCE 216:309-311(1982).
DR EMBL: J00493; G195007;
DR PIR: A02028; HVMG7.
DR HSP: P01789; SFAP.
KW IMMUNOGLOBULIN V REGION: ANTIAPSONATE ANTIBODY: HYBRIDOMA: SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).
FT NON_TER 140 140
SQ SEQUENCE 140 AA: 0790D5C8 CRC32:

Query Match 47.8% Score 454; DB 5: Length 140;
Best Local Similarity 56.3% Pred. No. 2.68e-78;
Matches 71: Conservative 23; Mismatches 27; Indels 5; Gaps 4;

Db 20 evqlqsgaeivkagssvkmcsksgyftfssygmwvkrpqgglewgiyngpqtany 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQLLESGSEVKKPGSSVKVSCPRASGSGFSPSYNFWVPQAPGQGLEWMGGIIPMFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 80 nekfgkttltvdkssstaysmqlrsltsedsavycarsh--yyg-gs-yd-fdywqgt 134
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AQKFGQGVITTADESTATGYMELSLSPSEDTAVYICAMPYKHCPSGSGWGFDPWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 135 pltvss 140
:|||||:
QY 121 LVTYSS 126

RESULT 8
ID HV50_MOUSE STANDARD: PRT: 120 AA.
AC P06329:
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (AC38 15.3).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
RN EUTHERIA: RODENTIA
RN [1]
RP SEQUENCE.
RX MEDLINE: 84182519.
RA DILDROP P, ROVENS J, SIEKEVITZ M, REYENHEIP K, RAJENSKY K.
RL EMBL J. 3:517-523(1984).
DR PIR: A02037; MMS15.
DR HSP: P01772; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA: 85EC01BA CRC32:

Query Match 47.0% Score 446; DB 5: Length 120;
Best Local Similarity 53.2% Pred. No. 1.98e-76;
Matches 67: Conservative 25; Mismatches 28; Indels 6; Gaps 5;

Db 1 qvqlqsgaeivkagssvkmcsksgyftfssygmwvkrpqgglewgiyngpqtany 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQLLESGSEVKKPGSSVKVSCPRASGSGFSPSYNFWVPQAPGQGLEWMGGIIPMFGTANY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 nekfgkttltvdkssstaysmqlrsltsedsavycarsh--yyg-gs-yd-fdywqgt 114
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AQKFGQGVITTADESTATGYMELSLSPSEDTAVYICAMPYKHCPSGSGWGFDPWGQGT 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 115 pltvss 120
:|||||:
QY 121 LVTYSS 126

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FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 134 IH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; DER2C7DA CPC32;

Query Match 46.9%; Score 445; DB 5; Length 139;
Best Local Similarity 54.0%; Pred.No.3.39e-76;
Matches 68; Conservative 27; Mismatches 25; Indels 6; Gaps 4;

Db 20 qvqlgqpaelvkvgaavklsckasgytflidyymwvkvqrgqlgwlgrldpnsgotky 79
QY 1 EVQLLESEFVKKPKSSVKVSCPASGGSFSTFNFNVPKAPQGGLEWVGGIIPMGITANY 60

Db 80 nekfkskatlvtvkpsataymqllssltedsavvyccar-y-dyy--gs--syfdywdqgt 133
QY 61 AKQFGQVTTIADESTATGYMELSSIPSEPTAVVYCAMPYPKHCSGSGCWGFDPWQGT 120

Db 134 tltyss 139
QY 121 LTVSS 126

RESULT 11
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (AC38 205.12).
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE.
FX MEDLINE: 84182519.
RA DILDRQP R, BOVENS J., STEKEVITZ M, REYPERTHEP K, PAJEWSKY K ;
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MHMS38.
DR HSP. P01772. IFGV.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 2DICE77 CPC32;

Query Match 46.5%; Score 441; DB 5; Length 118;
Best Local Similarity 57.0%; Pred.No.2.90e-75;
Matches 57; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

Db 1 evqlgqpaelvkvgaavklsckasgytflidyymwvkvqshaksrlgwlqldinnpgatsy 60
QY 1 EVQLLESEFVKKPKSSVKVSCPASGGSFSTFNFNVPKAPQGGLEWVGGIIPMGITANY 60

Db 61 ngkfkxkatltvdksstatymclrsitssedsavvyccargy 100
QY 61 AKQFGQVTTIADESTATGYMELSSLRSEDTAVVYCAMPY 100

RESULT 12
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (MOPC 104E).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE.

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[illegible]

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Db 1 evqlqsgpelvkgasvkmcskasytftdyymkwvkqshgkalewigdinpnngttsy 60
QY 1 EVQLLESGSEVKKPGSSVKVSCRASGGSEFRSYNPNWVRQAPQGGLWMGGIIPMEGTANY 60
Db 61 ndkfkgkatltvdksstaymqlnsltsedsavyyca----rd--r--yw-yfdvwaagt 111
QY 61 AOKFOGRVTITADESTATGYMELSSLRSEDTAIVYYCAMPYPKHCSRGSWGDFWGGGT 120
Db 112 tvtvss 117
QY 121 LVTVSS 126

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Search completed: Tue Feb 24 07:15:44 1998
 Job time : 19 secs.